

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:19:57 ; Search time 47 Seconds  
(without alignments)  
2012.955 Million cell updates/sec

Title: US-09-913-770B-1

Perfect score: 1798

Sequence: 1 MNFFHASCWNTSAELINKSW.....ORRATEKEINNMONTILKSHF 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1798	100.0	340	10	US-09-791-932-117
2	1798	100.0	340	10	US-09-990-940-2
3	1798	100.0	340	10	US-09-964-923A-2
4	1798	100.0	340	14	US-10-291-990-29
5	1798	100.0	340	14	US-10-321-807-40
6	1798	100.0	340	16	US-10-332-082-3
7	1793	99.7	340	10	US-09-971-269-4
8	1792	99.7	340	14	US-10-225-567A-666
9	1765	98.2	340	14	US-10-309-515-34
10	1765	98.2	340	14	US-10-291-990-2
11	1765	98.2	340	14	US-10-126-764-34
12	1755	97.6	340	14	US-10-309-515-36
13	1755	97.6	340	14	US-10-291-990-4
14	1755	97.6	340	14	US-10-126-764-36
15	1754.5	97.6	335	16	US-10-333-946-11

16	1751	97.4	340	14	US-10-291-990-26
17	1724	95.9	340	14	US-10-291-990-22
18	1718	95.6	340	14	US-10-291-990-24
19	1703	94.7	330	14	US-10-291-990-17
20	1699	94.5	330	14	US-10-291-990-18
21	1663	92.5	348	14	US-10-291-990-15
22	1659	92.3	348	14	US-10-291-990-16
23	1658	92.2	370	14	US-10-291-990-19
24	1654.5	92.0	385	14	US-10-291-990-20
25	1616	89.9	334	14	US-10-291-990-25
26	1613	89.7	346	14	US-10-291-990-21
27	1611	89.6	338	14	US-10-291-990-27
28	1607	89.4	360	14	US-10-291-990-28
29	1601	89.0	346	14	US-10-291-990-23
30	1589	88.4	334	14	US-10-291-990-34
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33	1588	88.3	330	14	US-10-126-764-39
34	1586	88.2	346	14	US-10-291-990-33
35	747.5	41.6	347	14	US-10-309-515-60
36	744.5	41.4	359	14	US-10-309-515-50
37	744.5	41.4	359	14	US-10-126-764-50
38	736	40.9	352	14	US-10-309-515-48
39	736	40.9	352	14	US-10-126-764-48
40	670.5	37.3	345	14	US-10-309-515-52
41	670.5	37.3	345	14	US-10-126-764-52
42	569.5	31.7	353	9	US-09-885-478-4
43	569.5	31.7	353	10	US-09-899-732-4
44	569.5	31.7	353	10	US-09-964-923A-9
45	569.5	31.7	353	12	US-10-341-751-4

#### ALIGNMENTS

#### RESULT 1

US-09-791-932-117

; Sequence 117, Application US/09791932

; Publication No. US20030003451A1

; GENERAL INFORMATION:

; APPLICANT: Vogeli, Gabriel

; APPLICANT: Parodi, Luis A.

; APPLICANT: Hiebsch, Ronald R.

; APPLICANT: Lind, Peter

; APPLICANT: Kaytes, Paul S.

; APPLICANT: Ruff, Valerie

; APPLICANT: Huff, Rita M.

; APPLICANT: Wood, Linda S.

; TITLE OF INVENTION: No. US20030003451A1 G Protein-Coupled Receptors Cross-Referer

; FILE REFERENCE: 00325.US1

; CURRENT APPLICATION NUMBER: US/09/791,932

; CURRENT FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/184,305

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,304

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,303

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,397

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,247

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/188,880

; PRIOR FILING DATE: 2000-03-13

; PRIOR APPLICATION NUMBER: 60/217,369

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/217,370

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/218,492

; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: 60/186,810

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/188,064

; PRIOR FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: 60/186,457  
 ; PRIOR FILING DATE: 2000-03-02  
 ; PRIOR APPLICATION NUMBER: 60/213,861  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: 60/194,344  
 ; PRIOR FILING DATE: 2000-04-03  
 ; PRIOR APPLICATION NUMBER: 60/218,337  
 ; PRIOR FILING DATE: 2000-07-14  
 ; NUMBER OF SEQ ID NOS: 184  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 117  
 ; LENGTH: 340  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-791-932-117

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 Best Local Similarity 100.0%; Pred. No. 1.9e-167;  
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 QY 1 MNPFFASCNWTSABLLNKNWKEFAYQTASVVDVTVILPSMIGIICSTGLVGNILIVFTII 60  
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 DB 241 VPKQRVMKLTQWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYGVYLSICLSYASS 300  
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 DB 301 INPFYILLSGNFQKRLPQIORRATEKEINNMGNTLKSHP 340

RESULT 2  
 US-09-990-940-2  
 ; Sequence 2, Application US/09990940  
 ; Publication No. US20030027252A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tian, Hui  
 ; APPLICANT: Zhao, Jiaqiang  
 ; APPLICANT: Chen, Jin-Long  
 ; APPLICANT: Cutler, Gene  
 ; APPLICANT: An, Songzhu  
 ; APPLICANT: Dai, Kang  
 ; APPLICANT: Gupta, Jamila S.  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: NO. US20030027252A1el Receptors  
 ; FILE REFERENCE: 018781-007410US  
 ; CURRENT APPLICATION NUMBER: US/09/990,940  
 ; CURRENT FILING DATE: 2001-11-21  
 ; PRIOR APPLICATION NUMBER: US 60/252,841  
 ; PRIOR FILING DATE: 2000-11-22  
 ; PRIOR APPLICATION NUMBER: US 60/257,636  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: US 60/261,377  
 ; PRIOR FILING DATE: 2001-01-12  
 ; PRIOR APPLICATION NUMBER: US 60/279,554  
 ; PRIOR FILING DATE: 2001-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/280,696  
 ; PRIOR FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 340  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGS342.  
 ; OTHER INFORMATION: melanin-concentrating hormone receptor 2 (NCHR2)  
 US-09-990-940-2

Query Match 100.0%; Score 1798; DB 10; Length 340;  
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 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPFFASCNWTSABLLNKNWKEFAYQTASVVDVTVILPSMIGIICSTGLVGNILIVFTII 60  
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 QY 181 VESCAFDLTSDDVLWYLYTITTTFFPLPLILVCHILCYTWEMYQONKARCCNPS 240  
 DB 181 VESCAFDLTSDDVLWYLYTITTTFFPLPLILVCHILCYTWEMYQONKARCCNPS 240  
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 DB 241 VPKQRVMKLTQWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYGVYLSICLSYASS 300  
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RESULT 3  
 US-09-964-923A-2  
 ; Sequence 2, Application US/09964923A  
 ; Publication No. US20030096300A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FEDER, J. N.  
 ; APPLICANT: MINTIER, G.  
 ; APPLICANT: RAMANATHAN, C. S.  
 ; APPLICANT: HAWKEN, D. R.  
 ; APPLICANT: CACACE, A.  
 ; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV9,  
 ; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND TESTES  
 ; FILE REFERENCE: D0045NP  
 ; CURRENT APPLICATION NUMBER: US/09/964,923A  
 ; CURRENT FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: 60/309,625  
 ; PRIOR FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: 60/261,775  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: 60/235,709  
 ; PRIOR FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 69  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 340  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-964-923A-2

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DB 121 SAIMTWSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
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US-10-291-990-29  
; Sequence 29, Application US/10291990  
; Publication No. US20030148457A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett Kinrade, Michele  
; APPLICANT: Brodbeck, Robbin M.  
; APPLICANT: Waters, Stephen  
; APPLICANT: Krause, James E.  
; TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors  
; FILE REFERENCE: N01.2102  
; CURRENT APPLICATION NUMBER: US/10/291,990  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 60/350,493  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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Best Local Similarity 100.0%; Pred. No. 1.9e-167;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPGLCTIITSIDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPGLCTIITSIDTCNQFAC 120  
QY 121 SAIMTWSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
DB 121 SAIMTWSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
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DB 181 VESCAFDLTSPDDVLYTYLTITTTFFFLPLILVCYIILCYTWEMYQONKDACCCNPS 240  
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DB 241 VPQRVWMLTKWLVLVVWVFLSAAAPHYIQLVNLQMEOPTAFYVGYLSICLSYASS 300  
QY 301 INPFLYILLSGNFQKRLPOIQRATEKEINNMGNTLKSHF 340  
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US-10-321-807-40  
; Sequence 40, Application US/10321807  
; Publication No. US20030166148A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Rupong  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Lowitz, Kevin P.  
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G  
; FILE REFERENCE: AREN0086  
; CURRENT APPLICATION NUMBER: US/10/321,807  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: US/09/714,008  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: PCT/US99/23938  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,088  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,099  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,369  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/171,902  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/171,901  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/171,900  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/181,749  
; PRIOR FILING DATE: 2000-02-11  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-321-807-40  
Query Match 100.0%; Score 1798; DB 14; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.9e-167;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPGLCTIITSIDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPGLCTIITSIDTCNQFAC 120  
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DB 121 SAIMTWSVDRYFALVQPFRLTRWRTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
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DB 181 VESCAFDLTSPDDVLYTYLTITTTFFFLPLILVCYIILCYTWEMYQONKDACCCNPS 240  
QY 241 VPQRVWMLTKWLVLVVWVFLSAAAPHYIQLVNLQMEOPTAFYVGYLSICLSYASS 300  
DB 241 VPQRVWMLTKWLVLVVWVFLSAAAPHYIQLVNLQMEOPTAFYVGYLSICLSYASS 300  
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RESULT 6
US-10-332-082-3
; Sequence 3, Application US/10332082
; Publication No. US20040086941A1
; GENERAL INFORMATION:
; APPLICANT: MORI, Masaaki;
; APPLICANT: SHIMOMURA, Yukio;
; APPLICANT: HARADA, Mioko;
; APPLICANT: SUGO, Tsukasa;
; APPLICANT: SHINTANI, Yasushi
; TITLE OF INVENTION: Method Screening MCH Receptor Antagonist/Agonist
; FILE REFERENCE: 2752 USOP
; CURRENT APPLICATION NUMBER: US/10/332,082
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: PCT/JP01/05809
; PRIOR FILING DATE: 2001-07-04
; PRIOR APPLICATION NUMBER: JP 2000-208254
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Human
US-10-332-082-3

Query Match      100.0%; Score 1798; DB 16; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.9e-167;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGGGLCTIITSLDTCNQFAC 120
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGGGLCTIITSLDTCNQFAC 120
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Db 121 SAIMTVMSVDRYFALVQPFRLTRWRTYKTRINLGLWAASFILALPWVYKVIKFDG 180
Qy 181 VESCAFDLTSPDDVLWTLVLTITTTFFPLILVLCVILCYTWEMYYQNKDARCCNPS 240
Db 181 VESCAFDLTSPDDVLWTLVLTITTTFFPLILVLCVILCYTWEMYYQNKDARCCNPS 240
Qy 241 VPKQVVKLTQWLVLVVVFILSAAPYHVIQVNLQWEOPTLAFYVGYLSICLSYASSS 300
Db 241 VPKQVVKLTQWLVLVVVFILSAAPYHVIQVNLQWEOPTLAFYVGYLSICLSYASSS 300
Qy 301 INPFLYLLSGNFQKRLPQIQRATEKEINNMGNLTAKSHF 340
Db 301 INPFLYLLSGNFQKRLPQIQRATEKEINNMGNLTAKSHF 340

RESULT 7
US-09-971-269-4
; Sequence 4, Application US/09971269
; Publication No. US20030148281A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 65499 AND 58875, NOVEL SEVEN
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS AND USES THEREOF
; FILE REFERENCE: ME100-414P1RM
; CURRENT APPLICATION NUMBER: US/09/971,269
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/237,700
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

Qy 1 MNPFCSCWNTSABLNNKSNKEFAYQTASVDTVILPMSMIGIICSTGLVGNILIVFTII 60
Db 1 MNPFCSCWNTSABLNNKSNKEFAYQTASVDTVILPMSMIGIICSTGLVGNILIVFTII 60
Qy 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGGGLCTIITSLDTCNQFAC 120
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGGGLCTIITSLDTCNQFAC 120
Qy 121 SAIMTVMSVDRYFALVQPFRLTRWRTYKTRINLGLWAASFILALPWVYKVIKFDG 180
Db 121 SAIMTVMSVDRYFALVQPFRLTRWRTYKTRINLGLWAASFILALPWVYKVIKFDG 180
Qy 181 VESCAFDLTSPDDVLWTLVLTITTTFFPLILVLCVILCYTWEMYYQNKDARCCNPS 240
Db 181 VESCAFDLTSPDDVLWTLVLTITTTFFPLILVLCVILCYTWEMYYQNKDARCCNPS 240
Qy 241 VPKQVVKLTQWLVLVVVFILSAAPYHVIQVNLQWEOPTLAFYVGYLSICLSYASSS 300
Db 241 VPKQVVKLTQWLVLVVVFILSAAPYHVIQVNLQWEOPTLAFYVGYLSICLSYASSS 300
Qy 301 INPFLYLLSGNFQKRLPQIQRATEKEINNMGNLTAKSHF 340
Db 301 INPFLYLLSGNFQKRLPQIQRATEKEINNMGNLTAKSHF 340

RESULT 8
US-10-225-567A-666
; Sequence 666, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 666
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (245)..(245)
; OTHER INFORMATION: Unknown Amino Acid
US-10-225-567A-666

Query Match      99.7%; Score 1792; DB 14; Length 340;
Best Local Similarity 99.7%; Pred. No. 7.3e-167;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNPFCSCWNTSABLNNKSNKEFAYQTASVDTVILPMSMIGIICSTGLVGNILIVFTII 60
Db 1 MNPFCSCWNTSABLNNKSNKEFAYQTASVDTVILPMSMIGIICSTGLVGNILIVFTII 60
Qy 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGGGLCTIITSLDTCNQFAC 120
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGGGLCTIITSLDTCNQFAC 120
Qy 121 SAIMTVMSVDRYFALVQPFRLTRWRTYKTRINLGLWAASFILALPWVYKVIKFDG 180
Db 121 SAIMTVMSVDRYFALVQPFRLTRWRTYKTRINLGLWAASFILALPWVYKVIKFDG 180
Qy 181 VESCAFDLTSPDDVLWTLVLTITTTFFPLILVLCVILCYTWEMYYQNKDARCCNPS 240
Db 181 VESCAFDLTSPDDVLWTLVLTITTTFFPLILVLCVILCYTWEMYYQNKDARCCNPS 240
Qy 241 VPKQVVKLTQWLVLVVVFILSAAPYHVIQVNLQWEOPTLAFYVGYLSICLSYASSS 300
Db 241 VPKQVVKLTQWLVLVVVFILSAAPYHVIQVNLQWEOPTLAFYVGYLSICLSYASSS 300
Qy 301 INPFLYLLSGNFQKRLPQIQRATEKEINNMGNLTAKSHF 340
Db 301 INPFLYLLSGNFQKRLPQIQRATEKEINNMGNLTAKSHF 340
```



QY 121 SAINTVMSVDRYPALVQPFRLTRWTRTYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180  
DB 121 SAINTVMSVDRYPALVQPFRLTRWTRTYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180  
QY 181 VESCAFDLTSDDVLMWTLVLTITTFPPFLPLILVCIILCYTWMYQONKDACCCNPS 240  
DB 181 VESCAFDLTSDDVLMWTLVLTITTFPPFLPLILVCIILCYTWMYQONKDACCCNPS 240  
QY 241 VPKQVWMLTKWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYVGYLSICLSYASSS 300  
DB 241 VPKQVWMLTKWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYVGYLSICLSYASSS 300  
QY 301 INPFYLLSGNFQKRLPQIORRATEKEINNMGNLTLSHF 340  
DB 301 INPFYLLSGNFQKRLPQIORRATEKEINNMGNLTLSHF 340

## RESULT 9

US-10-309-515-34  
; Sequence 34, Application US/10309515  
; Publication No. US20030114644A1

; GENERAL INFORMATION:  
; APPLICANT: Bennett Kinrade, Michele

; APPLICANT: Brodbeck, Robbin M.  
; APPLICANT: Waters, Stephen E.

; APPLICANT: Krause, James E.  
; TITLE OF INVENTION: Melanin Concentrating Hormone Receptors

; FILE REFERENCE: N00.2102C1  
; CURRENT APPLICATION NUMBER: US/10/309,515

; CURRENT FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/284,835

; PRIOR FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: 10/126,764

; PRIOR FILING DATE: 2002-04-18  
; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 34

; LENGTH: 340  
; TYPE: PRT

; ORGANISM: Macaca fascicularis  
US-10-309-515-34

Query Match 98.2%; Score 1765; DB 14; Length 340;  
Best Local Similarity 97.6%; Pred. No. 3.2e-164;  
Matches 332; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNPFFHSCWNTSAELNKSNNKEFAYQTASVVDVTILPMSIGIICSTGLVGNILIVFTII 60  
DB 1 MNPFFHSCWNTSAELNKSNNKEFAYQTASVVDVTILPMSIGIICSTGLVGNILIVFTII 60  
QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGPLCTIITSIDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGPLCTIITSIDTCNQFAC 120  
QY 121 SAINTVMSVDRYPALVQPFRLTRWTRTYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180  
DB 121 SAINTVMSVDRYPALVQPFRLTRWTRTYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180  
QY 181 VESCAFDLTSDDVLMWTLVLTITTFPPFLPLILVCIILCYTWMYQONKDACCCNPS 240  
DB 181 VESCAFDLTSDDVLMWTLVLTITTFPPFLPLILVCIILCYTWMYQONKDACCCNPS 240  
QY 241 VPKQVWMLTKWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYVGYLSICLSYASSS 300  
DB 241 VPKQVWMLTKWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYVGYLSICLSYASSS 300  
QY 301 INPFYLLSGNFQKRLPQIORRATEKEINNMGNLTLSHF 340  
DB 301 INPFYLLSGNFQKRLPQIORRATEKEINNMGNLTLSHF 340

## RESULT 10

US-10-291-990-2

; Sequence 2, Application US/10291990  
; Publication No. US20030148457A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett Kinrade, Michele  
; APPLICANT: Brodbeck, Robbin M.  
; APPLICANT: Waters, Stephen  
; APPLICANT: Krause, James E.  
; TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors  
; FILE REFERENCE: N01.2102  
; CURRENT APPLICATION NUMBER: US/10/291,990  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 60/350,493  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 340  
; TYPE: PRT  
; ORGANISM: Macaca fascicularis  
US-10-291-990-2

Query Match 98.2%; Score 1765; DB 14; Length 340;  
Best Local Similarity 97.6%; Pred. No. 3.2e-164;  
Matches 332; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNPFFHSCWNTSAELNKSNNKEFAYQTASVVDVTILPMSIGIICSTGLVGNILIVFTII 60  
DB 1 MNPFFHSCWNTSAELNKSNNKEFAYQTASVVDVTILPMSIGIICSTGLVGNILIVFTII 60  
QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGPLCTIITSIDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGPLCTIITSIDTCNQFAC 120  
QY 121 SAINTVMSVDRYPALVQPFRLTRWTRTYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180  
DB 121 SAINTVMSVDRYPALVQPFRLTRWTRTYKTIRINLGLWAASFILALPVWVYSKVIKFKDG 180  
QY 181 VESCAFDLTSDDVLMWTLVLTITTFPPFLPLILVCIILCYTWMYQONKDACCCNPS 240  
DB 181 VESCAFDLTSDDVLMWTLVLTITTFPPFLPLILVCIILCYTWMYQONKDACCCNPS 240  
QY 241 VPKQVWMLTKWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYVGYLSICLSYASSS 300  
DB 241 VPKQVWMLTKWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFYVGYLSICLSYASSS 300  
QY 301 INPFYLLSGNFQKRLPQIORRATEKEINNMGNLTLSHF 340  
DB 301 INPFYLLSGNFQKRLPQIORRATEKEINNMGNLTLSHF 340

## RESULT 11

US-10-126-764-34

; Sequence 34, Application US/10126764  
; Publication No. US20030166834A1

; GENERAL INFORMATION:  
; APPLICANT: Bennett Kinrade, Michele

; APPLICANT: Brodbeck, Robbin  
; APPLICANT: Krause, James

; TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS  
; FILE REFERENCE: N00.2102

; CURRENT APPLICATION NUMBER: US/10/126,764  
; CURRENT FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: 60/284,835  
; PRIOR FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Patent in version 3.1

; SEQ ID NO 34  
; LENGTH: 340

; TYPE: PRT  
; ORGANISM: Macaca fascicularis

US-10-126-764-34

Query Match 98.2%; Score 1765; DB 14; Length 340;



;; PRIOR APPLICATION NUMBER: 60/284,835  
;; PRIOR FILING DATE: 2001-04-19  
;; NUMBER OF SEQ ID NOS: 58  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 36  
;; LENGTH: 340  
;; TYPE: PRT  
;; ORGANISM: Macaca fascicularis  
US-10-126-764-36

Query Match 97.6%; Score 1755; DB 14; Length 340;  
Best Local Similarity 97.4%; Pred. No. 3.1e-163;  
Matches 331; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MNPFFHSCWNTSAELLNKSNNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60  
Db 1 MNPFFHSCWNTSAELLNKSNNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60  
QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVGGPLCTIITSLDTCNQFAC 120  
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVGGPLCTIITSLDTCNQFAC 120  
QY 121 SAIMTMSVDRYFALVQPFRLTSWRTYKTIIRINLGLWAASFILALPVMYISKVIFKDG 180  
Db 121 SAIMTMSVDRYFALVQPFRLTSWRTYKTIIRINLGLWAASFILALPVMYISKVIFKDG 180  
QY 181 VESCAFDLTSPDDVLWYTLTITTFPPFLPLILVVCYLILCYTWEMVQONKDCNPS 240  
Db 181 VESCAFDLTSPDDVLWYTLTITTFPPFLPLILVVCYLILCYTWEMVQONKDCNPS 240  
QY 241 VPQRVWKLTKMVLVAVFSLAAPHYIQLVNLQMEQPTLAFYVGYLSICLSYASS 300  
Db 241 VPQRVWKLTKMVLVAVFSLAAPHYIQLVNLQMEQPTLAFYVGYLSICLSYASS 300  
QY 301 INPFYLLSGNFQKRLPQIQRVTDKEIKNMGNTLKSHF 340  
Db 301 INPFYLLSGNFQKRLPQIQRVTDKEIKNMGNTLKSHF 340

RESULT 15  
US-10-333-946-11  
;; Sequence 11, Application US/10333946  
;; Publication No. US20040023252A1  
;; GENERAL INFORMATION:  
;; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.  
;; APPLICANT: REVIZU, Chandra S.; LAL, Preeti G.  
;; APPLICANT: BURFORD, Neil; YUE, Henry  
;; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.  
;; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.  
;; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.  
;; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.  
;; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.  
;; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam  
;; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.  
;; APPLICANT: LEE, Ernestine A.; DING, Li  
;; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS  
;; FILE REFERENCE: PI-0176 USN  
;; CURRENT APPLICATION NUMBER: US/10/333,946  
;; PRIOR FILING DATE: 2003-01-22  
;; PRIOR APPLICATION NUMBER: PCT/US01/23433  
;; PRIOR FILING DATE: 2001-07-25  
;; PRIOR APPLICATION NUMBER: US 60/221,478  
;; PRIOR FILING DATE: 2000-07-27  
;; PRIOR APPLICATION NUMBER: US 60/223,268  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: US 60/227,054  
;; PRIOR FILING DATE: 2000-08-21  
;; PRIOR APPLICATION NUMBER: US 60/231,121  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: US 60/232,243  
;; PRIOR FILING DATE: 2000-09-13  
;; PRIOR APPLICATION NUMBER: US 60/232,691  
;; PRIOR FILING DATE: 2000-09-15

;; PRIOR APPLICATION NUMBER: US 60/235,146  
;; PRIOR FILING DATE: 2000-09-22  
;; NUMBER OF SEQ ID NOS: 38  
;; SOFTWARE: PERL Program  
;; SEQ ID NO 11  
;; LENGTH: 335  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: Incyte ID No. US20040023252A1 55002225CD1  
US-10-333-946-11

Query Match 97.6%; Score 1754.5; DB 16; Length 335;  
Best Local Similarity 98.2%; Pred. No. 3.4e-163;  
Matches 334; Conservative 0; Mismatches 1; Indels 5; Gaps 1;  
QY 1 MNPFFHSCWNTSAELLNKSNNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60  
Db 1 MNPFFHSCWNTSAELLNKSNNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60  
QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVGGPLCTIITSLDTCNQFAC 120  
Db 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVGGPLCTIITSLDTCNQFAC 120  
QY 121 SAIMTMSVDRYFALVQPFRLTSWRTYKTIIRINLGLWAASFILALPVMYISKVIFKDG 180  
Db 121 SAIMTMSVDRYFALVQPFRLTSWRTYKTIIRINLGLWAASFILALPVMYISKVIFKDG 180  
QY 181 VESCAFDLTSPDDVLWYTLTITTFPPFLPLILVVCYLILCYTWEMVQONKDCNPS 240  
Db 181 VESCAFDLTSPDDVLWYTLTITTFPPFLPLILVVCYLILCYTWEMVQONKDCNPS 240  
QY 241 VPQRVWKLTKMVLVAVFSLAAPHYIQLVNLQMEQPTLAFYVGYLSICLSYASS 300  
Db 241 VPQRVWKLTKMVLVAVFSLAAPHYIQLVNLQMEQPTLAFYVGYLSICLSYASS 300  
QY 301 INPFYLLSGNFQKRLPQIQRVTDKEIKNMGNTLKSHF 340  
Db 301 INPFYLLSGNFQKRLPQIQRVTDKEIKNMGNTLKSHF 340

Search completed: May 13, 2004, 16:25:49  
Job time : 48 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:15:52 ; Search time 20 Seconds  
(without alignments)  
1635:256 Million cell updates/sec

Title: US-09-913-770B-1

Perfect score: 1798

Sequence: 1 MNPFHASCWNTSAELLNKS.....QRRATEKINNNGNTLKSHF 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1798	100.0	340	2 JC7695	G protein-coupled
2	565.5	31.5	422	2 JC7080	melanin-concentrat
3	468.5	26.1	363	2 I57940	somatostatin recep
4	456.5	25.4	418	2 A46226	somatostatin recep
5	449	25.0	391	2 A41795	somatostatin recep
6	449	25.0	391	2 C41795	somatostatin recep
7	449	25.0	391	2 A39297	somatostatin recep
8	441.5	24.6	428	2 S30508	probable G protein
9	440.5	24.5	428	2 A44021	somatostatin recep
10	438.5	24.4	369	2 JC2083	somatostatin recep
11	438	24.4	363	2 I57955	somatostatin recep
12	438	24.4	364	2 I57963	somatostatin recep
13	434	24.1	369	2 B41795	somatostatin recep
14	432.5	24.1	369	2 A45291	somatostatin recep
15	432.5	24.1	369	2 A41795	somatostatin recep
16	427.5	23.8	346	2 S29248	somatostatin recep
17	421.5	23.4	384	2 A47249	brain-specific som
18	418	23.2	388	2 I57965	somatostatin recep
19	417.5	23.2	380	2 S36143	kappa opioid recep
20	417.5	23.2	384	2 JC4629	somatostatin recep
21	416.5	23.2	380	2 A48227	kappa opioid recep
22	408.5	22.7	380	2 JC2434	kappa opioid recep
23	405.5	22.6	380	2 A55259	kappa opioid recep
24	403.5	22.4	380	2 JC2338	kappa opioid recep
25	395	22.0	372	2 S34592	delta opioid recep
26	394.5	21.9	372	2 I38532	delta opioid recep
27	394	21.7	372	2 B48227	delta opioid recep
28	390	21.7	398	2 I56517	mu opioid receptor
29	390	21.7	398	2 A57510	mu opioid receptor

30 389 21.6 398 2 I56504 mu opioid receptor  
31 388 21.6 400 2 I56553 mu opiate receptor  
32 387 21.5 392 2 S65693 opioid receptor mu  
33 381.5 21.2 373 2 JF0087 delta opioid recep  
34 359.5 20.0 367 2 I49022 kappa opioid recep  
35 359.5 20.0 367 2 JC2421 opioid receptor ho  
36 359.5 20.0 367 2 I56520 G protein-coupled  
37 356.5 19.8 370 2 S43087 orphan opioid rece  
38 355 19.7 328 2 I38973 G protein-coupled  
39 341.5 19.0 333 2 I38974 G protein-coupled  
40 327.5 18.3 425 2 A37912 thrombin receptor  
41 327.5 18.2 362 2 UN0694 angiotensin II rec  
42 319 17.7 411 2 I56444 thyrotrophin-relea  
43 319 17.7 412 2 S23436 thyrotrophin recep  
44 312.5 17.4 393 2 A39251 thyrotropin-releas  
45 310.5 17.3 398 2 JN0708 thyrotropin-releas

#### ALIGNMENTS

##### RESULT 1

JC7695

G protein-coupled receptor, SLT receptor - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 22-Oct-2001

C:Accession: JC7695

R:Mori, M.; Harada, M.; Terao, Y.; Sugo, T.; Watanabe, T.; Shimomura, Y.; Abe, M.; Shint

Biochem. Biophys. Res. Commun. 283, 1013-1018, 2001

A>Title: Cloning of a novel G protein-coupled receptor, SLT, a subtype of the melanin-c-

A:Reference number: JC7695; MUID:21255282; PMID:11355873

A:Contents: Hippocampus

A:Accession: JC7695

A:Molecule type: mRNA

A:Residues: 1-340 <MOR>

A:Cross-references: DBJ:AB060151

C:Comment: This receptor, a second subtype of the melanin-concentrating hormone (MCH) re

memory.

C:Genetics:

A:Gene: slt

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 100.0%; Score 1798; DB 2; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.5e-156;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPFHASCWNTSAELLNKSNNKEPAYQTASVVDTVILPSMIGITCSTGLVGNILIVFTII 60

DB 1 MNPFHASCWNTSAELLNKSNNKEPAYQTASVVDTVILPSMIGITCSTGLVGNILIVFTII 60

QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGGPLCTIIITSLDTCNOFAC 120

DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGGPLCTIIITSLDTCNOFAC 120

QY 121 SAIMTMSVDRYFALVQVFFRLTRWTRYKTRINLGLWAASFILALPWVYKVIKFDG 180

DB 121 SAIMTMSVDRYFALVQVFFRLTRWTRYKTRINLGLWAASFILALPWVYKVIKFDG 180

QY 181 VESCAFDLTSPDDVLYLVTITTEFFPLILVVCVILLCYTWEMVQONKDACCNPS 240

DB 181 VESCAFDLTSPDDVLYLVTITTEFFPLILVVCVILLCYTWEMVQONKDACCNPS 240

QY 241 VPKQVKNKLTKMWLVLVVVVILSAAPHYIQLVNLQMEQPTLAFYVGYISICLSYASSS 300

DB 241 VPKQVKNKLTKMWLVLVVVVILSAAPHYIQLVNLQMEQPTLAFYVGYISICLSYASSS 300

QY 301 INPPLYILLSGNFOKRLPQRRATEKEINNMGNTLKSHF 340

DB 301 INPPLYILLSGNFOKRLPQRRATEKEINNMGNTLKSHF 340

##### RESULT 2

A46226  
somatostatin receptor 3 - human  
C&Species: Homo sapiens (man)  
C&Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Nov-1999  
C&Accession: A46226; S32501  
R: Yamada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Seino, M.; Seino, M.  
Mol. Endocrinol. 6, 2136-2142, 1992  
A&Title: Somatostatin receptors, an expanding gene family: cloning and functional characterization  
A&Reference number: A46226; MUID:93149123; PMID:1337145  
A&Accession: A46226  
A&Molecule type: DNA  
A&Residues: 1-418 <YAM>  
A&Cross-references: GB:M96738; NID:G338498; PIN:AAA60592.1; PID:G338499  
A&Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIP:123690)  
R: Corness, J.D.; Demchayshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikanth, C.B.; Kent, G.A.; Febs Lett, 321, 279-284, 1993  
A&Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays preference for [D-Trp]Somatostatin  
A&Reference number: S32501; MUID:93238970; PMID:8097479  
A&Accession: S32501  
A&Status: preliminary  
A&Molecule type: DNA  
A&Residues: 1-418 <COR>  
C&Genetics:  
A&Gene: GDB:SSTR3  
A&Cross-references: GDB:134187; OMIM:182453  
A&Map position: 22q13.1-22q13.1  
A&Intons: #status absent  
C&Superfamily: vertebrate rhodopsin  
C&Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
F&44-70/Domains: transmembrane #status predicted <TM1>  
F&81-106/Domains: transmembrane #status predicted <TM2>  
F&118-139/Domains: transmembrane #status predicted <TM3>

F;339/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 25.0%; Score 449; DB 2; Length 391;  
Best Local Similarity 31.3%; Pred. No. 2.8e-33;  
Matches 102; Conservative 67; Mismatches 111; Indels 46; Gaps 9;

QY 35 VILPSMIGIICSTGLVGNLIVFTIR-SRKTVDPDIYICNLAVADLVHVGMPFLI--- 90  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
59 ILISFYSVCLVLGCNSMWIVILRYAKMKATNIYILNLAIDELLMLSPVPLTST 118  
QY 91 ---HOWARGGEWFGGPLECTIIITSLDTCNQFACSAIMTVMSVDYFALVPFRLTRWRTR 147  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
119 LLRH-----WPFGALLCRVLSDVANWNFTSIYCLTVLSVDYVAVVHPIKAARYRP 171  
QY 148 YKTI RNGLWAASFILALPWVYYSKVIFKGDSVCAPDLTSPPD--VLWYTLYLTIITT 205  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
172 TVAKVNLGWVLLSILVIPVFVSRTAANSDDGTVA CNLMPEAQRWLVGFVLYTF LMG 231  
QY 206 FFFPLPILVCIYLICYLT-----WMYQQNKDACRCNPSPVKQRVMKLTKMVLVLV 257  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
232 FLFPVGAICLCVLIIAKMHWALKAGWQ-QRKRSE-----KITLWMVMVU 277  
QY 258 VFVILSAAPHVQLVNLQMEOPTAFYGVGYLSICLSYASSINSINFLYILLSGNFQRL 317  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
278 MVFVICMWPYPVOLNVNFAEQDATV---SQLSVILGYANSCANPILYGLFSDFPKRSF 334  
QY 318 PQI-----QRRATEKEINNNGNTLS 338  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
335 QRILCSLWDNAAEFVDYYATAKS 360

RESULT 6  
C41795  
somatostatin receptor 1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-1993 #sequence\_revision 31-Dec-1993 #text\_change 24-Nov-1999  
C;Accession: C41795  
R;Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992  
A;Title: Cloning and functional characterization of a family of human and mouse  
A;Reference number: A41795; PMID:92108031; PMID:1346068  
A;Accession: C41795  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-391 <YAM>  
A;Cross-references: GB:M81831; NID:g201058; PIDN:AAAS8255.1; PID:g201059  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 25.0%; Score 449; DB 2; Length 391;  
Best Local Similarity 31.3%; Pred. No. 2.8e-33;  
Matches 102; Conservative 67; Mismatches 111; Indels 46; Gaps 9;

QY 35 VILPSMIGIICSTGLVGNLIVFTIR-SRKTVDPDIYICNLAVADLVHVGMPFLI--- 90  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
59 ILISFYSVCLVLGCNSMWIVILRYAKMKATNIYILNLAIDELLMLSPVPLTST 118  
QY 91 ---HOWARGGEWFGGPLECTIIITSLDTCNQFACSAIMTVMSVDYFALVPFRLTRWRTR 147  
Db : : : : ~~~~~~ WPFGALLCRVLSDVANWNFTSIYCLTVLSVDYVAVVHPIKAARYRP 171  
QY 148 YKTI RNGLWAASFILALPWVYYSKVIFKGDSVCAPDLTSPPD--VLWYTLYLTIITT 205  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
172 TVAKVN LGWVLLSILVIPVFVS RTAANS DDGTVA CNLMPE AQRWLV GFVLYTF LM 231  
QY 206 FFFPLPILVCIYLICYLT-----WMYQQNKDACRCNPSPVKQRVMKLTKMV LV 257  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
232 FLFPVGAICLCVLIIA KM HWAL KAGW Q-QRKR SE-----KITL W VMVU 277  
QY 258 VFVILSAAPHVQLVNLQMEOPTAFYGVGYLSICLSYASSINSINFLYILLSGNFQRL 317  
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
278 MVFVICMWPYPVOL NVNFA EQ DATV---SQL SV I LGY AN SCANI LY GL FS DF PK RSF 334

QY 318 PQI-----QRRATEKINNMGNLTLS 338  
 Db 335 QRILCLSWNDNAEEFVDYATALKS 360

RESULT 7  
 A39297  
 somatostatin receptor - rat  
 N:Alternate names: Probable G-protein-coupled receptor; SRIF receptor  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 03-Aug-1992 #sequence\_revision 03-Aug-1992 #text\_change 24-Nov-1999  
 C:Accession: A39297; A45102; S20088  
 R:Meyerhof, W.; Faust, H.J.; Schoenrock, C.; Richter, D.  
 DNA Cell Biol. 10, 689-694, 1991  
 A:Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed in brain  
 A:Reference number: A39297; MUID:92096119; PMID:1661599  
 A:Accession: A39297  
 A:Molecule type: mRNA  
 A:Residues: 1-391 <MEY>  
 A:CROSS-references: GB:X62314; GB:X61630; NID:G56309; PIDN:CAA44193.1; PID:G56310  
 A:Experimental source: brain  
 A:Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated at Met-2  
 R:Li, X.J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.  
 J. Biol. Chem. 267, 21307-21312, 1992  
 A:Title: Cloning and expression of a rat somatostatin receptor enriched in brain.  
 A:Reference number: A45102; MUID:93016064; PMID:1400442  
 A:Accession: A45102  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-391 <LI>  
 A:Experimental source: brain  
 A:Note: sequence extracted from NCBI backbone (NCBIP:116692)  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match 25.0%; Score 449; DB 2; Length 391;  
 Best Local Similarity 31.3%; Pred. No. 2.Be-33;  
 Matches 102; Conservative 67; Mismatches 111; Indels 46; Gaps 9;

QY 35 VILPSMTGIICSTGLVGNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMPFLI--- 90  
 Db 59 ILISFIYSVCLVGLCGSNVYVILRYAKMTATNIYILNLATADELLMSLPFLVTST 118

QY 91 ---HQWARGGEWVGGLCTIITSLDTCNQFACSAINTVMSVDYRYPALVOPFELTRWTR 147  
 Db 119 LLRH-----WPGALLCRVLSDVAVNMFTSYCTVLSVDYRYPALVOPFELTRWTR 171

QY 148 YKTIRINLGLWAASFILALPVWYYSKVIFKDGVCAPDLTGPDD--VLWYTLTYLTIT 205  
 Db 172 TVAKVNLGVWVLSLLVLPVIVFSTAAANSDDGTACNMLMPEPAQRWLVGFVLYTFLMG 231

QY 206 FFFPLPLILVCIILCYT-----WEMVQONKDRCCNPSVPKORVMKLTVMVLV 257  
 Db 232 FLLPVGALICLVLIHAKRMVALKAGMQ--QRRKSR-----KILMWMWVV 277

QY 258 VVFILSRAPHYIOLVNLQEQPTLAFVGVYLSICLSYASSSINPFYIILSGNFQRL 317  
 Db 278 MVFVLCWPFVYVQLVNVFAQDDATV---SQLSVILGYANSCANPILYGLFSDNPKRSF 334

QY 318 PQI-----QRRATEKINNMGNLTLS 338  
 Db 335 QRILCLSWNDNAEEFVDYATALKS 360

RESULT 8  
 S30508  
 probable G protein-coupled receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 11-Jan-2000  
 C:Accession: S30508  
 R:Meyerhof, W.; Wulfsen, I.; Schoenrock, C.; Fehr, S.; Richter, D.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 10267-10271, 1992  
 A:Title: Molecular cloning of a somatostatin-28 receptor and comparison of its expressed

A:Reference number: S30508; MUID:93066220; PMID:1279674

A:Accession: S30508

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-428 <MEY>

A:CROSS-references: EMBL:X63574; NID:G56315; PIDN:CAA45130.1; PID:G56316

A:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.6%; Score 441.5; DB 2; Length 428;

Best Local Similarity 31.8%; Pred. No. 1.5e-32;

Matches 108; Conservative 73; Mismatches 136; Indels 23; Gaps 10;

QY 1 MNPFA-SCHWTSAEELANKSWKEFAVOTASVDVTILPSMIGIICSTGLVGNILIVFTIIR 59

Db 14 LDPGNASSAMPDLSLGNASAGTSLA---GLAVSGILISLVLVVGVGLGNSLVIVV 70

QY 60 IR-SRKKTVPDIYICNLAVADLVHIVGMPFLIHOWARGGEWVGGLCTIITSLDTCNQF 118

Db 71 LRHTSSPSVTSVYILNLALADELFMLGLPFLAAQNAL-SYMPFGSLMCLRLVMAVDGINQF 129

QY 119 ACSAIMTMSVDYRYPALVOPFELTRWTRTYKTIRINLGLWAASFILALPVWYYSKVIFK 178

Db 130 TSIFCLTMSVDYRLAVVHPTRSAWRTPAPVARVMSAAVWVASAVVLPVVPVFGVPR-- 187

QY 179 DGVCAPDLTSPDVLWYTLTYLTIT---FFFLPLILVCIILCYLTWEMVQONKDR 235

Db 188 -GMSTCHNQWPEP-AAAWRTAFIYTAALGFGFLLVICLYLLIVKVRSTRVRAPS 245

QY 236 CNPSVP-----KORVMKLTVMVLVWVVFILSAAPHVITQLVNLQ---EOPFLAEVVG 287

Db 246 QWVQAPACQRRRRSRRVTRMVAVVALFVLCWMPFYLINLVNVCPLPEEP--APFGL 303

QY 288 YLSTCLSYASSINPFYIILSGNFQRLPQIQRRATEK 327

Db 304 YFLVVALPYANSCANPILYGLFSLYRFKQGFRLLRPSRR 343

# RESULT 9

A44021

somatostatin receptor SSTR3 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 11-Jan-2000

C:Accession: A44021

R:Yasuda, K.; Rens-Domiano, S.; Breder, C.D.; Law, S.F.; Saper, C.B.; Reisine, T.; Bell,

J. Biol. Chem. 267, 20422-20428, 1992

A:Title: Cloning of a novel somatostatin receptor, SSTR3, coupled to adenylylcyclase.

A:Reference number: A44021; MUID:93015924; PMID:1328199

A:Accession: A44021

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-428 <YAS>

A:CROSS-references: GB:M91000; NID:G201065; PIDN:AAA40144.1; PID:G201066

A:Note: sequence extracted from NCBI backbone (NCBIP:115746)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.5%; Score 440.5; DB 2; Length 428;

Best Local Similarity 31.8%; Pred. No. 1.8e-32;

Matches 107; Conservative 71; Mismatches 130; Indels 29; Gaps 9;

QY 3 PFASCHWTSAEELANKSWKEFAVOTASVDVTILPSMIGIICSTGLVGNILIVFTIIR- 61

Db 24 PLDTLTGNISAG-----ASLTGLAVSGILISLVLVVGVGLGNSLVIVVLRH 73

QY 62 SRKKTVPDIYICNLAVADLVHIVGMPFLIHOWARGGEWVGGLCTIITSLDTCNQFACS 121

Db 74 TSSPSVTSVYILNLALADELFMLGLPFLAAQNAL-SYMPFGSLMCLRLVMAVDGINQFTSI 132

QY 122 AITMVTMSVDYRYPALVOPFELTRWTRTYKTIRINLGLWAASFILALPVWYYSKVIFKDG 181

Db 133 FCLTMSVDYRLAVVHPTRSAWRTPAPVARVMSAAVWVASAVVLPVVPVFGVPR--GM 189



```
QY 182 ESCAFDLTSPDVLWYT---LYLTITTFRRPLILVLCYTWEMVQONKQARCCN 238
Db 190 STCHQWPEP-AAARWTAFIYMAALGFGLJVLICYLIVVVKVSTTRVAPSQW 248
QY 239 PSVP-----KQVMKLTQVLLVVLVVFILSAAPHYVQLVNLQW---EQPTLAFVGYL 290
Db 249 VQAPACQRRRSRSTRVWVAVVAVLFCWMPYLLNIVVCPLEEP--AFFGLYFL 306
QY 291 SICLSYASSINPFLYLILSGNFQKRLPQIQRATEK 327
Db 307 VVALPYANSCANPILYGLSTRFKQGRFRILLRPSRR 343

RESULT 10
JC2083
somatostatin receptor 2 - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 21-Jul-2000
C/Accession: JC2083
R;Matsumoto, K.; Yokogoshi, Y.; Fujinaka, Y.; Zhang, C.; Saito, S.
Biochem. Biophys. Res. Commun. 199, 298-305, 1994
A;Title: Molecular cloning and sequencing of porcine somatostatin receptor 2+.
A;Reference number: JC2083; MUID:94168590; PMID:8123027
A;Accession: JC2083
A;Molecule type: DNA
A;Residues: 1-369 <MAT>
A;Cross-references: GB:D21338; NID:9415606; PIDN:BAA04810.1; PID:9472306
C;Comment: This protein inhibits growth hormone release.
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; receptor
F;44-69/Domain: transmembrane #status predicted <TM1>
F;77-105/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;158-182/Domain: transmembrane #status predicted <TM4>
F;205-235/Domain: transmembrane #status predicted <TM5>
F;254-286/Domain: transmembrane #status predicted <TM6>
F;292-316/Domain: transmembrane #status predicted <TM7>
F;9,22,29,32/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;115-193/Disulfide bonds: #status predicted
F;244,343/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #
F;250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
F;328/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 24.4%; Score 438.5; DB 2; Length 369;
Best Local Similarity 31.8%; Pred. No. 2.4e-32;
Matches 103; Conservative 63; Mismatches 139; Indels 19; Gaps 8;

QY 2 NPFFASQWNTSAELLNKSWNKEFAYQATASVVDVILPSPMIGIICSTGLVGNILVFTIIR 61
Db 17 SPFDL---NGSVATANSNQTEPYDLTS---NAVTFYFVVCILGCLNTLIVITLIR 70
QY 62 -SRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGVWFGPLCTIITSLDTCNQFAC 120
Db 71 YAKRKITITNIYILNLAIDELEMLGLPFLAMQVAL-VHWPFGKACIRVWTVGDIQNQFTS 129
QY 121 SAITWMSVDVRYFALVQPFRLTWRTRYKTIRNLGLWAASFILALPVWVYSKVYKFDG 180
Db 130 IFCLTWMSIDRYLAVVHPYKSAKRRPRRTAKMINVAVGWSLLVILPIMYAGLSNQWG 189
QY 181 VESCAFDLTSPDVLWYT---LYLTITTFRRPLILVLCYTWEMVQONKQARCC 237
Db 190 RSSCTINWPG-ESGAVTGFIIYAFILGFLVPLTICLCYLFII-----IKVSGSIRV 242
QY 238 NPSVPKQVMKLTQVLLVVLVVFILSAAPHYVQLVNLQW-OTPLAFVGYLISLUSY 296
Db 243 GSKRRKKEKKVTRMYSVIVAVFICWLPFYIPNVSSVGA-SPTPALKGMDFVWVLTLY 302
QY 297 ASSSINPFLYLILSGNFQKRLPQI 320
Db 303 ANSCANPILYAFISDNFKKSPQNV 326

RESULT 11
```

I57955

somatostatin receptor - human

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 24-Nov-1999

C/Accession: I57955

R;Panetta, R.; Greenwood, M.T.; Warszynska, A.; Demchishyn, L.L.; Day, R.; Niznik, H.B.

Mol. Pharmacol. 45, 417-427, 1994

A;Title: Molecular cloning, functional characterization, and chromosomal localization of

A;Reference number: I57955; MUID:94195267; PMID:7908405

A;Accession: I57955

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-363 &lt;RES&gt;

A;Cross-references: GB:I14865; NID:9431094; PIDN:AAA20828.1; PID:9431095

C;Genetics:

A;Gene: GDB:SST

A;Cross-references: GDB:I19604; OMIM:182450

A;Map position: 3q28-3q28

C;Superfamily: vertebrate rhodopsin

Query Match 24.4%; Score 438; DB 2; Length 363;

Best Local Similarity 35.6%; Pred. No. 2.6e-32;

Matches 104; Conservative 58; Mismatches 110; Indels 20; Gaps 8;

QY 35 VILPSMIGIICSTGLVGNILVFTIIR-SRKKTVPDIYICNLAVADLVHVGMPFLIHQW 93

Db 41 VLVPVLYLLVCAAGLGGLTLYVYVLRFAKMTVTNIVILNLAVADLVHVGMPFLATQN 100

QY 94 ARGGSWVFGPLCTIITSLDTCNQFACSAIMTVMSVDVRYFALVQPFRLTRWRTRYKTIRI 153

Db 101 A-ASFWPFGPVLCLRWMLTDGVNQPTSVFCLTVMSVDVRYFALVQPFRLTRWRTRYKTIRI 159

QY 154 NLGLWAASFILALPVWVYSKVYKFDGVECAFDLTSPDDV-LW---YTLVLTITTFRRP 209

Db 160 SAAAWVLSLWSLPLLV-----FADVQEGTCHASWEPVGLWCAVFIITAVLGFPAP 213

QY 210 LPLILVYILLCYTWEMVQONKQARCCNPSPKQVMKLTQVLLVVLVVFILSAAPYHV 269

Db 214 LLVILCLCYLLIIV---KVRAAGVRVGC---VRRSRKVTQVWLVVVLVVFAGCWLPPFT 266

QY 270 IQVLNQLQEQTLAFYVG-YVLSICLSYASSINPFLYLILSGNFQKRLPQI 320

Db 267 VNIVNLAVLPQEPASAGLYFFVILSYANSCANPVLVYGLFSLDNFROSFQKV 318

RESULT 12

JN0763

somatostatin receptor 5 - human

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 20-Jun-2000

C/Accession: JN0763

R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I.

Biochem. Biophys. Res. Commun. 195, 844-852, 1993

A;Title: Cloning, functional expression and pharmacological characterization of a fourth

A;Reference number: JN0762; MUID:93384611; PMID:8373420

A;Accession: JN0763

A;Molecule type: DNA

A;Residues: 1-364 &lt;YAM&gt;

A;Cross-references: DDBJ:D16827; NID:9487683; PIDN:BAA04107.1; PID:9487684

C;Comment: This protein is a member of somatostatin receptor family.

C;Genetics:

A;Gene: GDB:SSSTR5

A;Cross-references: GDB:I138452; OMIM:182455

A;Map position: 16p13.3-16p13.3

A;Introns: #status absent

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; lipoprotein; phosphoprotein; thiol

F;40-66/Domain: transmembrane #status predicted &lt;TM1&gt;

F;77-102/Domain: transmembrane #status predicted &lt;TM2&gt;

F;114-135/Domain: transmembrane #status predicted &lt;TM3&gt;

F;155-177/Domain: transmembrane #status predicted &lt;TM4&gt;

F;196-228/Domain: transmembrane #status predicted &lt;TM5&gt;

F;246-273/Domain: transmembrane #status predicted &lt;TM6&gt;



Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992  
A;Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors  
A;Reference number: A41795; MUID:92108031; PMID:1346068  
A;Accession: D41795  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-369 <YAM>  
A;Cross-references: GB:M81832; NID:G201060; PIDN:AAAS8256.1; PID:G201061  
R;Elliot, D.E.; Metwalli, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstein, J.V.  
J. Immunol. 153, 1180-1186, 1994  
A;Title: T lymphocytes isolated from the hepatic granulomas of schistosome-infected mice  
A;Reference number: I56236; MUID:94300079; PMID:7913111  
A;Accession: I56236  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 99-309 <RES>  
A;Cross-references: GB:S71756; NID:G560631  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

Query Match 24.1%; Score 432.5; DB 2; Length 369;  
Best Local Similarity 31.9%; Pred. No. 8.Se-32;  
Matches 94; Conservative 63; Mismatches 125; Indels 13; Gaps 6;

QY 31 VVDTVILPSMIGIICSTGLVGNILIVFTIIR-SRKKTVDPDIKICNLAVADLVHIVGMPEL 89  
DB 40 MTSNAVLTFIYFVVCVGLCENTLVIVILRYAKMTIITNIIYILNIAIDELFMLGLPEL 99  
QY 90 IHQWARGGEVFGGPICTIITSLDTCNQFACSAIMTVMSVDYFALVQPFRLTRWRTRYK 149  
DB 100 AMQVAL-VHWPFGKACRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPKSAKWRPRPT 158  
QY 150 TIRINGLVAASFILALPVWYSKVYKFDGVESCAPDLTSPDDVLWYT---LYLTITTF 206  
DB 159 AKMINVAVMCVSLVILPIMYAGLSNQWGRSSCTINWPG-ESGAWYTGFIYAFILGF 217  
QY 207 FFPLPLILVCYILILCYTWEMYQNKDKARCCNPSPVKQKWKLTQWLVLVVVVFTLSAAP 266  
DB 218 LVPLTILICLYLFI-----IKVSSGIRVGSSEKKSEKVKTRNVSIVVAVFICWLP 271  
QY 267 YHVIQVNLQME-OPTLAFYGVYLSICLSYASSSINPFYILLGNFQKRLPQI 320  
DB 272 FYIFNVSSVSAISPTPALKGMFDFVILTYSANPILYAFSLDNFKKSPQNV 326

Search completed: May 13, 2004, 16:20:27  
JOB time : 21 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:09:06 ; Search time 18 Seconds  
(without alignments)  
983.547 Million cell updates/sec

Title: US-09-913-770B-1  
Perfect score: 1798  
Sequence: 1 MNPFASWNTSRELLKSW.....QRRATEKBNMGNLTKSHF 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141691 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141691

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1798	100.0	340	1 MCR2_HUMAN	Q969V1 homo sapien
2	1763	98.1	340	1 MCR2_MACMU	Q8mj88 macaca mula
3	1760	97.9	340	1 MCR2_MACFA	Q8sq54 macaca fasc
4	569.5	31.7	360	1 MCR1_RAT	P97639 rattus norv
5	569.5	31.7	423	1 MCR1_MOUSE	Q8j212 mus musculu
6	568.5	31.6	388	1 MCR1_MACMU	Q8mj89 macaca mula
7	565.5	31.5	422	1 MCR1_HUMAN	Q99705 homo sapien
8	468.5	26.1	363	1 SSR2_RAT	P30938 rattus norv
9	458.5	25.5	362	1 SSR5_MOUSE	O08858 mus musculu
10	456.5	25.4	418	1 SSR3_HUMAN	P32745 homo sapien
11	449	25.0	391	1 SSR1_HUMAN	P30872 homo sapien
12	449	25.0	391	1 SSR1_MOUSE	P30873 mus musculu
13	449	25.0	391	1 SSR1_RAT	P28846 rattus norv
14	442	24.6	368	1 SSR2_BOVIN	P34993 bos taurus
15	441.5	24.6	428	1 SSR2_RAT	P30936 rattus norv
16	440.5	24.5	428	1 SSR3_MOUSE	P30935 mus musculu
17	438.5	24.4	369	1 SSR2_PIG	P34994 sus scrofa
18	438	24.4	364	1 SSR5_HUMAN	P35346 homo sapien
19	434	24.1	369	1 SSR2_HUMAN	P30874 homo sapien
20	432.5	24.1	369	1 SSR2_MOUSE	P30875 mus musculu
21	432.5	24.1	369	1 SSR2_RAT	P30880 rattus norv
22	421.5	23.4	384	1 SSR4_RAT	P30937 rattus norv
23	418	23.2	388	1 SSR4_HUMAN	P31391 homo sapien
24	417.5	23.2	380	1 OPRK_RAT	P34975 rattus norv
25	417.5	23.2	384	1 SSR4_MOUSE	P49660 mus musculu
26	416.5	23.2	380	1 OPRK_MOUSE	P33534 mus musculu
27	405.5	22.6	380	1 OPRK_CAVPO	P41144 cavia porce
28	403.5	22.4	380	1 OPRK_HUMAN	P41145 homo sapien
29	396.5	22.1	372	1 OPRD_HUMAN	P41143 homo sapien
30	395	22.0	372	1 OPRD_RAT	P33533 rattus norv
31	394	21.9	372	1 OPRD_MOUSE	P32300 mus musculu
32	394	21.9	401	1 OPRM_PIG	Q95247 sus scrofa
33	392	21.8	401	1 OPRM_BOVIN	P79350 bos taurus

## ALIGNMENTS

### RESULT 1

ID	MCR2_HUMAN	STANDARD;	PRT;	340 AA.
AC	Q969V1; Q9BXA8;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Melanin-concentrating hormone receptor 2 (MCH receptor 2) (MCH2R-2)			
DE	(MCH-R2) (MCH2R) (MCH2) (G protein coupled receptor 145)			
DE	(GPRV17).			
GN	GPRI45 OR MCH2R OR SLT.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21255282; PubMed=11355873;			
RA	Mori M., Harada M., Terao Y., Sugo T., Watanabe T., Shimomura Y.,			
RA	Abe M., Shintani Y., Onda H., Nishimura O., Fujino M.;			
RT	"Cloning of a novel G protein-coupled receptor, SLT, a subtype of the			
RT	melanin-concentrating hormone receptor.";			
RT	Biochem. Biophys. Res. Commun. 283:1013-1018 (2001).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Fetal brain;			
RX	MEDLINE=21309932; PubMed=11404457;			
RA	Sailer A.W., Sano H., Zeng Z., McDonald T.P., Pan J., Pong S.-S.,			
RA	Feighner S.D., Tan C.P., Fukami T., Iwaasa H., Hreniuk D.L.,			
RA	Morin N.R., Sadowski S.J., Ito M., Ito M., Bansal A., Ky B.,			
RA	Figuerola D.J., Jiang Q., Austin C.P., MacNeil D.J., Ishihara A.,			
RA	Ihara M., Kanatani A., Van der Ploeg L.H.T., Howard A.D., Liu Q.;			
RT	"Identification and characterization of a second melanin-concentrating			
RT	hormone receptor, MCH-2R.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:7564-7569 (2001).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=21433976; PubMed=11459838;			
RX	Wang S., Behan J., O'Neill K., Weig B., Fried S., Laz T., Bayne M.,			
RA	Gustafson E., Hawes B.E.;			
RT	"Identification and pharmacological characterization of a novel human			
RT	melanin-concentrating hormone receptor, MCH-R2.";			
RT	J. Biol. Chem. 276:34664-34670 (2001).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=21282939; PubMed=11274220;			
RX	Hill J., Duckworth M., Muddock P., Rennie G., Sabido-David C.,			
RA	Ames R.S., Szekeres P., Wilson S., Bergema D.J., Gloger I.S.,			
RA	Lewy D.S., Chambers J.K., Muir A.I.;			
RT	"Molecular cloning and functional characterization of MCH2, a novel			
RT	human MCH receptor.";			
RT	J. Biol. Chem. 276:20125-20129 (2001).			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,			
RA	Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuho Y.,			

P42866 mus musculu  
P33535 rattus norv  
P35372 homo sapien  
Q9mvt9 macaca mula  
P35377 mus musculu  
P35370 rattus norv  
P47748 cavia porce  
P79292 sus scrofa  
P41146 homo sapien  
P48145 homo sapien  
Q8mjv3 bos taurus  
P48146 homo sapien

RA Furuichi K.;  
RT "Molecular characterization of a novel melanin-concentrating hormone  
RL receptor: evidence of its expression in lateral hypothalamus";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to G  
CC proteins that activate phosphoinositide hydrolysis.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Specifically expressed in the brain, with  
CC highest levels in cerebral cortex, hippocampus and amygdala. No  
CC expression detected in the cerebellum, thalamus or hypothalamus.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; AB060151; BAB55677.1; -  
CC EMBL; AY029596; AAK38157.1; -  
CC EMBL; AF399937; AAL05528.1; -  
CC EMBL; AF347063; AAK32193.1; -  
CC EMBL; AB058849; BAB7842.1; -  
CC PIR; JC7835; JC7695  
CC Genew; HGNC:20867; GPR145.  
CC  
CC MIN; 606111; -  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC InterPro; IPR008362; MCH2\_receptor.  
CC InterPro; IPR008361; MCH2\_receptor.  
CC Pfam; PF00001; 7tm.1.1.  
CC PRINTS; PR00237; GPCR\_Rhodopsin.  
CC PRINTS; PR01784; MCH2RECEPTOR.  
CC PRINTS; PR01783; MCH2RECEPTOR.  
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL2; 1.  
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC DOMAIN 1 39  
CC 1 (POTENTIAL)  
CC TRANSMEM 40 60  
CC DOMAIN 61 69  
CC 2 (POTENTIAL)  
CC TRANSMEM 70 90  
CC DOMAIN 91 104  
CC 3 (POTENTIAL)  
CC TRANSMEM 105 129  
CC DOMAIN 130 154  
CC 4 (POTENTIAL)  
CC TRANSMEM 155 175  
CC DOMAIN 176 200  
CC 5 (POTENTIAL)  
CC TRANSMEM 201 221  
CC DOMAIN 222 252  
CC 6 (POTENTIAL)  
CC TRANSMEM 253 273  
CC DOMAIN 274 288  
CC 7 (POTENTIAL)  
CC TRANSMEM 289 309  
CC DOMAIN 310 340  
CC CYTOPLASMIC (POTENTIAL)  
CC N-LINKED (GLCNAc...) (POTENTIAL)  
CC CARBOHYD 10 10  
CC 17  
CC N-LINKED (GLCNAc...) (POTENTIAL)  
CC CARBOHYD 17 17  
CC SEQUENCE 340 AA; 38849 MW; 754302B951FAC6 CRC64;  
Query Match 100.0%; Score 1798; DB 1; Length 340;  
Best Local Similarity 100.0%; Pred. No. 1.6e-119;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNPFCWNTSALLNKNWKEFAYQTASVVDVILPSMIGIICSTGLVGNLIVETII 60  
Db 1 MNPFCWNTSALLNKNWKEFAYQTASVVDVILPSMIGIICSTGLVGNLIVETII 60  
QY 61 RSRKKTVDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGGLPCTIITSLDTCNQFAC 120  
Db 61 RSRKKTVDIYICNLAVADLVHIVGMPFLIHQWARGGEVFGGLPCTIITSLDTCNQFAC 120  
QY 121 SAIMTVMSVDYFALVQPFRLTRWRYKTRINLGLWAASFIILALPWVYSKVIKFDG 180  
Db 121 SAIMTVMSVDYFALVQPFRLTRWRYKTRINLGLWAASFIILALPWVYSKVIKFDG 180

QY 181 VESCAFDLTSPDDVLTWTLTITTFPEPLPLILVCYVILLCYTWYQNKDARCCNPS 240  
Db 181 VESCAFDLTSPDDVLTWTLTITTFPEPLPLILVCYVILLCYTWYQNKDARCCNPS 240  
QY 241 VPKQRVKMLTKQVLVVLVVFILSAAPYHVIVQLVNLQEQPTLAFYVGYIYLSICLSYASS 300  
Db 241 VPKQRVKMLTKQVLVVLVVFILSAAPYHVIVQLVNLQEQPTLAFYVGYIYLSICLSYASS 300  
QY 301 INPFLYLLSNFQKRLPOIORRATERKEINNMGNLTKSHF 340  
Db 301 INPFLYLLSNFQKRLPOIORRATERKEINNMGNLTKSHF 340  
RESULT 2  
MCR2 MACMU STANDARD; PRT; 340 AA.  
AC Q8MU88;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Melanin-concentrating hormone receptor 2 (MCH receptor 2) (MCHR-2)  
DE (MCH-R2) (MCH2R) (MCH-2R) (MCH2) (G protein coupled receptor 145).  
GN GPR145 OR MCHR2  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fried S., O'Neill K., Hawes B.E.;  
RT "Cloning and characterization of rhesus monkey MCH-R1 and MCH-R2";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Tan C.P., Sano H., Iwase H., Pan J., Sailer A., Hreniuk D.L.,  
RA Feigener S.D., Palyna O.C., Figueroa D.J., Austin C.P., Jiang M.M.,  
RA Yu H., Ito M., Ito M., Guan X.M., Kanatani A.,  
RA Van der Ploeg L.H.T., Howard A.D.;  
RT "Melanin-concentrating hormone receptor subtypes 1 and 2: species  
specific gene expression";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to G  
CC proteins that activate phosphoinositide hydrolysis.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Specifically expressed in the brain with  
CC highest levels in cerebral cortex, hippocampus and hypothalamus,  
CC and lower levels in caudate nucleus, putamen and thalamus.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; AY078246; AAL80004.1; -  
CC EMBL; AF513989; AAM49794.1; -  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC InterPro; IPR008362; MCH2\_receptor.  
CC InterPro; IPR008361; MCH2\_receptor.  
CC Pfam; PF00001; 7tm.1.1.  
CC PRINTS; PR00237; GPCR\_Rhodopsin.  
CC PRINTS; PR01784; MCH2RECEPTOR.  
CC PRINTS; PR01783; MCH2RECEPTOR.  
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL2; 1.  
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein.  
CC DOMAIN 1 34  
CC 1 (POTENTIAL)  
CC TRANSMEM 35 57  
CC DOMAIN 58 69  
CC CYTOPLASMIC (POTENTIAL)

FT TRANSMEM 70 92 2 (POTENTIAL).  
FT DOMAIN 93 106 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 107 129 3 (POTENTIAL).  
FT DOMAIN 130 149 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 150 172 4 (POTENTIAL).  
FT DOMAIN 173 198 5 (POTENTIAL).  
FT TRANSMEM 199 221 6 (POTENTIAL).  
FT DOMAIN 222 252 7 (POTENTIAL).  
FT TRANSMEM 253 272 8 (POTENTIAL).  
FT DOMAIN 273 286 9 (POTENTIAL).  
FT TRANSMEM 287 309 10 (POTENTIAL).  
FT DOMAIN 310 340 11 (POTENTIAL).  
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 340 AA; 38783 MW; 17AC576C6F8FA758 CRC64;

Query Match 98.1%; Score 1763; DB 1; Length 340;  
Best Local Similarity 97.1%; Pred. No. 4.5e-117;  
Matches 330; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MNPFFHSCWNTSABLNSKNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60  
Db 1 MNPFFHSCWNTSABLNSKNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60

Qy 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWFGGPGPLCTIITSLDTCNQFAC 120  
Db 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWFGGPGPLCTIITSLDTCNQFAC 120

Qy 121 SAINTVMSVDVRYFALVQPFELTWRTRYKIRINLGLWAASFILALPVWYISKVKFDG 180  
Db 121 SAINTVMSVDVRYFALVQPFELTWRTRYKIRINLGLWAASFILALPVWYISKVKFDG 180

Qy 181 VESCAFDLTSPDDVWLYTLITTTFFPLPLVLCYILCYTWEMYOQNKDARCCNPS 240  
Db 181 VESCAFDLTSPDDVWLYTLITTTFFPLPLVLCYILCYTWEMYOQNKDARCCNPS 240

Qy 241 VPQRVMKLTQWLVLVAVFVLSAAPHVLIQVNLQWEOPTLAFYVGYVYISICLSYASS 300  
Db 241 VPQRVMKLTQWLVLVAVFVLSAAPHVLIQVNLQWEOPTLAFYVGYVYISICLSYASS 300

Qy 301 INPFLYLLSGNFQKRLPQIQRRTATEKEINNMGNTLKSHP 340  
Db 301 INPFLYLLSGNFQKRLPQIQRRTATEKEINNMGNTLKSHP 340

RESULT 3  
MCR2\_MACFA STANDARD; PRT; 340 AA.  
ID MCR2\_MACFA  
AC Q8S054;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Melanin-concentrating hormone receptor 2 (MCH receptor 2) (MCHR-2)  
DE (MCH-R2) (MCHR2) (MCH-2R) (MCH2) (G protein coupled receptor 145)  
DE (GPRV17).  
GN GPR145 OR MCHR2.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OC NCBI\_Taxid=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kurama T., Matsumoto S., Takasaki J., Terai K., Matsumoto M.,  
RA Kamohara M., Saito T., Soga T., Saito Y., Oda T., Masuho Y.,  
RA Furuchi K.;  
RT Molecular characterization of a novel melanin-concentrating hormone  
RT receptor: evidence of its expression in lateral hypothalamus.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to  
CC G proteins that activate phosphoinositide hydrolysis.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL AB058850; BAB87843.1;  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC InterPro; IPR008362; MCH2\_Receptor.  
CC InterPro; IPR008361; MCH\_Receptor.  
CC Pfam; PF00001; 7tm\_1; 1.  
CC PRINTS; PR00237; GPCR\_HODOPSIN.  
CC PRINTS; PR01784; MCH2RECEPTOR.  
CC PRINTS; PR01783; MCHRECEPTOR.  
CC PROSITE; PS00337; G-PROTEIN RECEPTOR F1.1; 1.  
CC PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 57 1 (POTENTIAL).  
FT DOMAIN 58 69 2 (POTENTIAL).  
FT TRANSMEM 70 92 3 (POTENTIAL).  
FT DOMAIN 93 106 4 (POTENTIAL).  
FT TRANSMEM 107 129 5 (POTENTIAL).  
FT DOMAIN 130 149 6 (POTENTIAL).  
FT TRANSMEM 150 172 7 (POTENTIAL).  
FT DOMAIN 173 198 8 (POTENTIAL).  
FT TRANSMEM 199 221 9 (POTENTIAL).  
FT DOMAIN 222 252 10 (POTENTIAL).  
FT TRANSMEM 253 272 11 (POTENTIAL).  
FT DOMAIN 273 286 12 (POTENTIAL).  
FT TRANSMEM 287 309 13 (POTENTIAL).  
FT DOMAIN 310 340 14 (POTENTIAL).  
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 340 AA; 38769 MW; BD2CF1972332439 CRC64;

Query Match 97.9%; Score 1760; DB 1; Length 340;  
Best Local Similarity 97.1%; Pred. No. 7.2e-117;  
Matches 330; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MNPFFHSCWNTSABLNSKNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60  
Db 1 MNPFFHSCWNTSABLNSKNKEFAYQTASVVDTVILPMSMIGIICSTGLVGNILIVFTII 60

Qy 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWFGGPGPLCTIITSLDTCNQFAC 120  
Db 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWFGGPGPLCTIITSLDTCNQFAC 120

Qy 121 SAINTVMSVDVRYFALVQPFELTWRTRYKIRINLGLWAASFILALPVWYISKVKFDG 180  
Db 121 SAINTVMSVDVRYFALVQPFELTWRTRYKIRINLGLWAASFILALPVWYISKVKFDG 180

Qy 181 VESCAFDLTSPDDVWLYTLITTTFFPLPLVLCYILCYTWEMYOQNKDARCCNPS 240  
Db 181 VESCAFDLTSPDDVWLYTLITTTFFPLPLVLCYILCYTWEMYOQNKDARCCNPS 240

Qy 241 VPQRVMKLTQWLVLVAVFVLSAAPHVLIQVNLQWEOPTLAFYVGYVYISICLSYASS 300  
Db 241 VPQRVMKLTQWLVLVAVFVLSAAPHVLIQVNLQWEOPTLAFYVGYVYISICLSYASS 300

Qy 301 INPFLYLLSGNFQKRLPQIQRRTATEKEINNMGNTLKSHP 340  
Db 301 INPFLYLLSGNFQKRLPQIQRRTATEKEINNMGNTLKSHP 340

RESULT 4  
MCR1\_RAT  
ID MCR1\_RAT  
AC P97639;  
DT 01-NOV-1997 (Rel. 35, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1)  
 DE (MCH-R1) (MCHIR) (MCHR-1R) (MCHR) (G protein coupled receptor 24)  
 DE (Somatostatin receptor-like protein) (SLC-1) (Fragment).  
 GN GPR24 OR MCHR1 OR SLC1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=98193144; PubMed=9531978;  
 RA Lakaye B., Minet A., Zorzi W., Grisar T.;  
 RT "Cloning of the rat brain cDNA encoding for the SLC-1 G protein-  
 RT coupled receptor reveals the presence of an intron in the gene.";  
 RL Biochim. Biophys. Acta 1401:216-220(1998).  
 RN [2]  
 RP SEQUENCE OF 150-307 FROM N.A.  
 RN MEDLINE=97131607; PubMed=8977118;  
 RA Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,  
 RA Cheng R., Heng H.H.O., George S.R., O'Dowd B.F.;  
 RT "Characterization of a human gene related to genes encoding  
 RT somatostatin receptors.";  
 RL FEBS Lett. 398:253-258(1996).  
 RN [3]  
 RP FUNCTION.  
 RN MEDLINE=20032718; PubMed=10559938;  
 RA Lembo P.M.C., Grazzini E., Cao J., Hubatsch D.A., Pelletier M.,  
 RA Hoffert C., Sc-Ong S., Pou C., Jabsque J., Groblewski T.,  
 RA O'Donnell D., Payza K., Ahmad S., Walker P.;  
 RT "The receptor for the orexigenic peptide melanin-concentrating hormone  
 RT is a G-protein-coupled receptor."  
 RL Nat. Cell Biol. 1:267-271(1999).  
 RN [4]  
 RP FUNCTION.  
 RN MEDLINE=99347736; PubMed=10421368;  
 RA Saito Y., Notthacker H.P., Wang Z., Lin S.H., Leslie F., Civelli O.;  
 RA "Molecular characterization of the melanin-concentrating-hormone  
 RT receptor."  
 RL Nature 400:265-269(1999).  
 CC -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to  
 CC G proteins that inhibit adenylyl cyclase.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: High level in the brain, moderate amounts  
 CC in the eye and skeletal muscle, and small amounts in tongue and  
 CC pituitary.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 -----  
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 -----  
 DR EMBL; AF008650; AAC27977.1; -;  
 DR EMBL; U77953; AAC14588.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR InterPro; IPR004647; MCH1\_Receptor.  
 DR InterPro; IPR008361; MCH\_Receptor.  
 DR Pfam; PF00001; 7tm1; 1.  
 DR PRINTS; PR00237; GPCR\_RHODOPSN.  
 DR PRINTS; PR01507; MCHIRRECEPTOR.  
 DR PRINTS; PR01783; MCHRECEPTOR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; FALSE\_NEG.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F2\_1;  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1  
 FT NON\_TER <1 52  
 FT TRANSMEM 53 73  
 FT EXTRACELLULAR (POTENTIAL).  
 FT 1 (POTENTIAL).

FT DOMAIN 74 86  
 FT TRANSMEM 87 107  
 FT DOMAIN 108 125  
 FT TRANSMEM 126 146  
 FT DOMAIN 147 168  
 FT TRANSMEM 169 189  
 FT DOMAIN 190 211  
 FT TRANSMEM 212 232  
 FT DOMAIN 233 263  
 FT TRANSMEM 264 284  
 FT DOMAIN 285 301  
 FT TRANSMEM 302 322  
 FT DOMAIN 323 360  
 FT CARBOHYD 20 20  
 FT CARBOHYD 23 23  
 FT CARBOHYD 30 30  
 SQ SEQUENCE 360 AA; 39727 MW; B68D3C993E491350 CRC64;  
 Query Match 31.7%; Score 569.5; DB 1; Length 360;  
 Best Local Similarity 36.7%; Pred. No. 2.8e-33;  
 Matches 114; Conservative 60; Mismatches 114; Indels 23; Gaps 4;  
 QY 35 VILPSMGIICSTGLVGNILIVFTIIRSK-----KTPVDIYICNLAVDLVHVGMPFLI 90  
 DB 48 IIMPVSFGTICLLGIVGNSTVIFAVKRSKLRWCNSNPDEIFINLSVDLLFLGMPFMI 107  
 QY 91 HQWARGGEWFGGPLCTIITSLDTCNQFACSAIMTVMSVDYRYPALVQPFELTRWRTRYKT 150  
 DB 108 HOLMGNGVWHFGETMCTLIITAMDANSQFTSTYILTAMTIDRYLATVHPISSTKFRKPSMA 167  
 QY 151 IRINLGLWAASFIILPWWYSKVIKFGVESCADFLTSPD-DVLWYLYLTITITFFPP 209  
 DB 168 TLVTCLLWALSFSITPFWLYARLIPPGGAVCGGIRLNPDPDLWYLYOFFLAFALP 227  
 QY 210 LPLILVCVYLITLCYTWEMYOQNKDARCNPSV-----KQVWKLTQKVLVVLVVVFIIS 263  
 DB 228 FVVTAAVVKIL-----QRMSTVSPASQSRIRLTKRVTRTAICLVFFVC 275  
 QY 264 AAPHVQLVNLQNEQTLAPYGVYLSICLSYASSINPFYLLSGNFQKRLPOIQRR 323  
 DB 276 WAPYVQLTQLSISRPTLTFLVLYNAAISGLVANSCLNPFYVIVLCETFRKRLVSLVKP 335  
 QY 324 ATEKEINNMGN 334  
 DB 336 AAQQLRTVSN 346  
 RESULT 5  
 MCHR1\_MOUSE  
 ID MCHR1\_MOUSE STANDARD; PRT; 423 AA.  
 AC Q8VZL2;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Melanin-concentrating hormone receptor 1 (MCH receptor 1) (MCHR-1)  
 DE (MCH-R1) (MCHIR) (MCHR-1R) (MCHR) (G protein coupled receptor 24)  
 DE (Somatostatin receptor-like protein) (SLC-1).  
 DE GPR24 OR MCHR1 OR SLC1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 71-423 FROM N.A.  
 RC STRAIN=129/SVJ;  
 RA Lakaye B., Adamantidis A., Coumans B., Zorzi W., Parmentier M.,  
 RA Grisar T.;  
 RT "Cloning of the mouse melanin-concentrating hormone receptor 1 gene  
 RT and promoter characterization."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 71-423 FROM N.A.  
 RN STRAIN=ILS, and ISS;  
 RC



DR	PRINTS; PR01507; MCHLRRECEPTOR.
DR	PRINTS; PR01783; MCHRECEPTOR.
DR	PROSITE; PS00237; G PROTEIN RECP F1_1; FALSE_NEG.
DR	PROSITE; PSS0262; G PROTEIN RECP F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.
FT	DOMAIN 1 114 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 115 137 1 (POTENTIAL)
FT	DOMAIN 138 149 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 150 172 2 (POTENTIAL).
FT	DOMAIN 173 186 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 187 209 3 (POTENTIAL).
FT	DOMAIN 210 229 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 230 252 4 (POTENTIAL).
FT	DOMAIN 253 279 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 280 302 5 (POTENTIAL).
FT	DOMAIN 303 322 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 323 345 6 (POTENTIAL).
FT	DOMAIN 346 359 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 360 382 7 (POTENTIAL).
FT	DOMAIN 383 423 CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 83 83 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT	CARBOHYD 86 86 N-LINKED (GLCNAC.. ) (POTENTIAL).
FT	CARBOHYD 93 93 N-LINKED (GLCNAC.. ) (POTENTIAL).
SQ	SEQUENCE 423 AA; 46269 MW; 9E26A7DB9D494569 CRC64;
Query Match	31.7%; Score 569.5; DB 1; Length 423;
Best Local Similarity	36.7%; Pred. No. 3.2e-33;
Matches 114; Conservative 60; Mismatches 114; Indels 23; Gaps 4;	
QY	35 VILPSMIGICTSLVGNLIVFTIRSRK---KTVPDIYICNLAVDLHVHVGPFLLI 90 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
Db	111 IIMPSVFETICLLGIIGNSTVIFAVVYKKSLHWCSNVDIFITINSWDLLFLFGMPFMI 170 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
QY	91 HOWARGEWEVGGPCLTILTSDTNCOFACSALMTVMVSVDRYFALVQPRLTFWRTRYKT 150 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
Db	171 HQLMGVWHFGFMTCMLTLITAMDANSQFTSYLTATAMADRVLATVHPISSTFKRKPSMA 230 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
QY	151 IRINGLWAASFILPVWMVYSKVIKFDGVSFCAPDLTSPP-DVLWTLYLTITTTFFFP 209 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
Db	231 TLVICLLWALSFSITPWLVLYEARLIFFPGAGCGGIRLPNDTDLYWFXYOFFLAFLP 290 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
QY	210 LPFILLVCYLIIICYWEMYQQNKDARCNPSPV-----KQVKLTKEVLVLVVVFILLS 263 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
Db	291 FVVTAAAYKYIL-----QRMTSSVAPASQRSIRLTRKVRTTAIAICLVFFVC 338 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
QY	264 AAPHYVIOVLWNLOMEOPTLAFYVGYVLSICLSYASSINPFYVILLSGNFOKRPOIQRR 323 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
Db	339 WAPYYVQLQTQSISEPTLFITYLNAILSYANCLNPFYVIVLCETFRRKLVLVSKP 398 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
QY	324 AYEKENNNGN 334 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
Db	399 AAQGQLRTVSN 409 : ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  :
RESULT 6	
MCR1_MACMU	STANDARD; PRT; 388 AA.
ID	MCR1 MACMU
AC	Q8MJ89;
DT	10-OCT-2003 (Rel. 42, Created)
DT	10-OCT-2003 (Rel. 42, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Melanin-concentrating hormone receptor 1 (MCHR-receptor 1) (MCHR-1)
DE	(MCH-R1) (MCHR-1R) (MCHR) (G protein coupled receptor 24)
DE	(Fragment).
OS	GPR24 OR MCHR1.
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC	Cercopithecinae; Macaca.
OX	NCBIXTaxID=9544;
RX	[1]
RA	Tan C.P., Sano H.A.
RA	Pan J., Sailer A., Hreniuk D.L.



RA Scott C.B., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
RA Williams C.L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuoyama S.,  
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,  
RA Fulton R., Johnson D., Benis G., Bentley D., Bradshaw H., Bourne S.,  
RA Cordes M., Du Z., Fulton L., Goele D., Graves T., Hawkins J.,  
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
RA Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.,  
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,  
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.B.,  
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
RA Khan A.S., Lane L., Tilahun Y., Wright H.,  
RT "The DNA sequence of human chromosome 22.",  
RL Nature 402:489-495(1999).  
[5]  
RN SEQUENCE FROM N.A., AND VARIANT ASP-32.  
RP TISSUE=Brain;  
RC MEDLINE=22398257; PubMed=12477932;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Casavant G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Munzy D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettum A.C., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,  
RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.",  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[6]  
RN SEQUENCE OF 77-422 FROM N.A.  
RX MEDLINE=97131607; PubMed=8977118;  
RA Kolakowski L.F. Jr., Jung B.P., Nguyen T., Johnson M.P., Lynch K.R.,  
RA Cheng R., Heng H.H.Q., George S.R., O'Dowd B.F.,  
RT "Characterization of a human gene related to genes encoding  
somatostatin receptors.",  
RL FEBS Lett. 398:253-258(1996).  
[7]  
RN FUNCTION  
RX MEDLINE=99347735; PubMed=10421367;  
RA Chambers J., Ames R.S., Bergsma D., Muir A., Fitzgerald L.R.,  
RA Hervieu G., Dytko G.M., Foley J.J., Martin J., Liu W.S., Park J.,  
RA Ellis C., Ganguly S., Konchar S., Cluderay J., Leslie R., Wilson S.,  
RA Sarau H.M.,  
RT "Melanin-concentrating hormone is the cognate ligand for the orphan  
G-protein-coupled receptor SLG-1.",  
RL Nature 400:261-265(1999).  
CC -!- FUNCTION: Receptor for melanin-concentrating hormone, coupled to  
both G proteins that inhibit adenylyl cyclase and G proteins that  
activate phosphoinositide hydrolysis.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Highest level in brain, particularly in the

frontal cortex and hypothalamus, lower levels in the liver and heart.  
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
-!- CAUTION: It is uncertain whether Met-1, Met-6 or Met-70 is the initiator.  
-!- CAUTION: Ref.4 and Ref.6 sequences differ from that shown due to erroneous gene model prediction.  
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-----  
CC EMBL; AB063174; BAB0890.1; -  
CC EMBL; AF490537; AA014670.1; -  
CC EMBL; BT006725; AAP35371.1; -  
CC EMBL; Z86090; CAB62343.1; ALT\_SEQ.  
CC EMBL; BC001736; AAH01736.1; -  
CC EMBL; BC021146; AAH21146.1; -  
CC EMBL; U71092; AAC14587.1; ALT\_SEQ.  
CC PIR; JC7080; JC7080.  
CC Genew; HGNC:4479; GPR24.  
CC XIM; 601751; -  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
CC GO; GO:0008188; F:neuropeptide receptor activity; TAS.  
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.  
CC GO; GO:0006091; P:energy pathways; TAS.  
CC GO; GO:0007631; P:feeding behavior; TAS.  
CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. ; TAS.  
CC GO; GO:0007193; P:G-protein signaling, adenylylate cyclase inhi. ; TAS.  
CC InterPro; IPR000276; GPCR\_Rhoopsn.  
CC InterPro; IPR004047; MCH1\_receptor.  
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCRHDOPSN.  
CC PRINTS; PR01507; MCHRECEPTOR.  
CC PRINTS; PR01783; MCHRECEPTOR.  
CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; FALSE\_NEG.  
CC PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Polymorphism; Glycoprotein.  
FT DOMAIN 1 113  
FT TRANSMEM 114 136  
FT DOMAIN 137 148  
FT TRANSMEM 149 171  
FT DOMAIN 172 185  
FT TRANSMEM 186 208  
FT DOMAIN 209 227  
FT TRANSMEM 228 250  
FT DOMAIN 251 278  
FT TRANSMEM 279 301  
FT DOMAIN 302 321  
FT TRANSMEM 322 344  
FT DOMAIN 345 358  
FT TRANSMEM 359 381  
FT DOMAIN 382 422  
FT CARBOHYD 82 82  
FT CARBOHYD 85 85  
FT CARBOHYD 92 92  
FT VARIANT 32 32  
SQ SEQUENCE 422 AA; 45962 MW; 3986919A18183818 CRC64;  
Query Match 31.5%; Score 565.5; DB 1; Length 422;  
Best Local Similarity 36.3%; Pred. No. 6.1e-33;  
Matches 113; Conservative 61; Mismatches 114; Indels 23; Gaps 4;  
OY 35 VILPSMIGICSTGLVGNILVFTIIRSK-----KTVPDIVICNLAVDLVHVGMPFLI 90  
DB 110 IIMSVFETICLLGIIGNSTVIFAVVKSKLHCNWNVPDIFINLSVDLLFLGLGPFMI 169

QY 91 HQWARGGEVFGGLCTIITSLDTCNQFACSAINTVMSVDYFALVQPFRLTRWRTRYKT 150  
 Db 170 HOLMGNGVHFGTMCITLITANDANSQFTSTYILTAMADRYLATVHPITSSTKFKPSVA 229  
 QY 151 IRINLGLWAASFILALPVWYVKIFKDVESCAFDLSPD-DVLWYLYLTITITFFFP 209  
 Db 230 TLVICLLWALSFSITSEWLYARLIPFGGAVGGRILNPDTLDYWFYLOFFLAFALP 289  
 QY 210 LPLILVCYIILCYTWEMYQONKDCARCNPSV-----KQVMKLTQVVLVWVVFILS 263  
 Db 290 FVITRAYVIL-----QMTSSVAPASORSIRLTKVTRTAIAICLVFFVC 337  
 QY 264 AAPHVQLNQLQEQTLAFYGVYLSICLSVASSINPFLYILISGNFQKRLPOIQRR 323  
 Db 338 WAPYVYLQTLQISRTPLTVLYLNAALISGVANSCLNPFVYIVLCFTRKRLVLSVRP 397  
 QY 324 ATEKEINMGN 334  
 Db 398 AAQQLRAVSN 408

RESULT 8  
 SSR5 RAT  
 ID \_SSR5 RAT STANDARD; PRT; 363 AA.  
 AC P30938;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Somatostatin receptor type 5 (SSR5).  
 GN Rattus norvegicus (Rat).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pituitary;  
 RX MEDLINE=9312549; PubMed=1362243;  
 RA O'Carroll A.-M., Lolait S.J., Konig M., Mahan L.C.;  
 RT "Molecular cloning and expression of a pituitary somatostatin  
 receptor with preferential affinity for somatostatin-28.";  
 RL Mol. Pharmacol. 42:939-946(1992).  
 RN (2)  
 RP REVISIONS TO C-TERMINUS.  
 RC TISSUE=Pituitary;  
 RX MEDLINE=94195267; PubMed=7908405;  
 RA Panetta R., Greenwood M.T., Warszynska A., Demchishyn L.L., Day R.,  
 RA Niznik H.B., Srikant C.B., Patel Y.C.;  
 RT "Molecular cloning, functional characterization, and chromosomal  
 localization of a human somatostatin receptor (somatostatin receptor  
 type 5) with preferential affinity for somatostatin-28.";  
 RL Mol. Pharmacol. 45:417-427(1994).  
 CC -!- FUNCTION: Receptor for somatostatin-28. The activity of this  
 CC receptor is mediated by G proteins which inhibit adenylyl cyclase.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Prominent in the pituitary and small  
 CC intestine. Low levels in islets and spleen. Not detected in  
 CC kidney, pancreas, cerebellum, or cortex.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; L04535; AAA17029.1; -  
 CC EMBL; U01152; AAC09011.1; -  
 CC EMBL; X74828; CAA52825.1; -  
 CC PIR; I57940; I57940.

DR HSP; P02699; 1888.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1 1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Lipoprotein; Palmitate.  
 FT DOMAIN 1 35  
 FT TRANSMEM 36 63  
 FT TRANSMEM 64 73  
 FT DOMAIN 74 99  
 FT TRANSMEM 100 111  
 FT DOMAIN 112 133  
 FT TRANSMEM 134 155  
 FT DOMAIN 156 176  
 FT TRANSMEM 177 196  
 FT DOMAIN 197 221  
 FT TRANSMEM 222 247  
 FT DOMAIN 248 273  
 FT TRANSMEM 274 283  
 FT DOMAIN 284 308  
 FT TRANSMEM 309 363  
 FT DOMAIN 364 380  
 FT CARBOHYD 13 13  
 FT CARBOHYD 23 23  
 FT CARBOHYD 186 186  
 FT DISULFID 110 185  
 FT LIPID 320 320  
 FT SEQUENCE 363 AA; 39971 MW; 48D4512960613B4A CRC64;  
 SQ  
 Query Match 26.1%; Score 468.5; DB 1; Length 363;  
 Best Local Similarity 35.3%; Pred. No. 3.5e-26;  
 Matches 114; Conservative 70; Mismatches 112; Indels 27; Gaps 11;  
 QY 9 WNTSNELL-NKSNKEFAVQATSVVD--TVLPSSMIGICSTGLVGNLIVFTIIRSK- 64  
 Db 12 WNASAASSGNHWS---LVGSASPMGARVLPVLYLVCTVGLSGNTLYIVVLRK 68  
 QY 65 KTVPDYICNLAVADLVHIVGMPELIHQWARGGEVFGGLCTIITSLDTCNQFACSAIM 124  
 Db 69 KIVTNVYILNLAVADLVPLMLGLPFLATQNAVSVYMPFGSFLCRVMTLDGNGQTSIFCL 128  
 QY 125 TVMSVDYFALVQPFRLTRWRTRYKTINLGLWAASFILALPVWYVKIFKDVESV 184  
 Db 129 VMMSVDYFALVQPFRLTRWRTRYKTINLGLWAASFILALPVWYVKIFKDVESV 185  
 QY 185 AFDLTSPDDV-LWYLYLTITIT---FFPPLILVLCVYILCYTWEMYQONKDCARCNPS 240  
 Db 186 --NLSSWPEVGLNGAFTYTVSLGFGPLVLCVYILVVKVKAAGMRVGSRR----- 238  
 QY 241 VKQRMKLTQVVLVWVVFILSAPYHVIQVNLQM---EPTLAFVGVYILSILSYA 297  
 Db 239 --RRSEPKVTRMVMVVVVLVFGVCLPFPFIVNINVLAFPLPEPTSAGL--YFVVVLSYA 295  
 QY 298 SSINPFIYLLSGNFKRLPOI 320  
 Db 296 NSCANPLLYGLSDNFRQSPKRV 318

RESULT 9  
 SSR5 MOUSE  
 ID \_SSR5 MOUSE STANDARD; PRT; 362 AA.  
 AC O08558; O08998;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Somatostatin receptor type 5 (SSR5).  
 GN SSTR5 OR SSTR5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN (1)

Matches	112;	Conservative	68;	Mismatches	103;	Indels	33;	Gaps	11;
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YY	19	SNWKEFAYOTA	---	SVVD	-----TWILPESMIGIICSTGLVGNLIVFTIIR-SRKKT	66
		:::	:	:	:::	:
db	11	SNWSAASGSHNSLVDPSPVMGARAVLPVLVLLCTVGLGNTLVIVYVLYAKVK	70			
		:::	:	:	:::	:
YY	67	VPIIYCINLAVADIHVHVGMPFLHOWARGGEWFGGPLCTIIISLDTCNQFACSAIMTV	126			
		:::	:	:	:::	:
db	71	VTNVYLNLNLAADVLFMLGLPFLATONA-VSYWPFGSFLCLVNLTLDGINQF	129			
		:::	:	:	:::	:
YY	127	MSVDRYFALVQPFRLTRWRTRYKTRINLGILWAASFILALPVWVYSKVIFKDGVESCAF	186			
		:::	:	:	:::	:
db	130	MSVDREVLAVVHPLRSGARWRPRVAKLASAAVVVSLLMSJPLLAFADV	--QEKGWGT	--	184	
		:::	:	:	:::	:
YY	187	DUTSPDDV-LWTYLLTITTT	----	PFPLPLILVCYIILLCTVEMYQNKDARCNPSPV	242	
		:::	:	:	:::	:
db	185	NLSWPEFPGVLGAAPITTSVLGFFGPILVITCLCYLLIVVKVKAAGMRVGSRR	----	R	238	
		:::	:	:	:::	:
YY	243	KQRWKMLTKWLVLVVVFILSAAAPHVIOLNLQM	----	EOPTLAFYGYVYLISCLSVASS	299	
		:::	:	:	:::	:
db	239	RRSERKVTENVVVVLVFGCWLFPFFVINVLAFTELPPEETSAGL	----	YFFVVVLSTANS	296	
		:::	:	:	:::	:
YY	300	SINPLYILLSGNFQK	315			
		:::	:	:	:::	:
db	297	CANPLYGLFSDFNQ	312			
		:::	:	:	:::	:

  

RESULT 10	SSR3_HUMAN	STANDARD;	PRT; 418 AA.
D C D C	SSR3_HUMAN	PRT; 418 AA.	
D C	P32745;		
T T	01-OCT-1993 (Rel. 27, Created)		
T T	01-OCT-1993 (Rel. 27, Last sequence update)		
T T	15-MAR-2004 (Rel. 43, Last annotation update)		
E E	Somatostatin receptor type 3 (SSR3) (SSR-28).		
N N	SSR3.		
N S	Homo sapiens (Human).		
C C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
X X	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
C X	NCBI_TaxID=9606;		
N P	SEQUENCE FROM N.A.		
X X	MEDLINE=93149123; PubMed=1337145;		
A A	Yamada Y., Reisine T., Law S.F., Ihara Y., Kubota A., Kagimoto S.,		
A A	Seino M., Seino Y., Bell G.I., Seino S.;		
T T	"Somatostatin receptors, an expanding gene family: cloning and		
T T	functional characterization of human SSR3, a protein coupled to		
T T	adenylyl cyclase";		
L L	Mol. Endocrinol. 6:2136-2142(1992).		
N N	[2]		
N P	SEQUENCE FROM N.A.		
X X	MEDLINE=93238970; PubMed=8097479;		
A A	Corness J.D., Deemshyn L.L., Seeman P., van Tol H.H.M.,		
A A	Srikant C.B., Kent G., Patel Y.C., Miznik H.B.;		
T T	"A human somatostatin receptor (SSR3), located on chromosome 22,		
T T	displays preferential affinity for somatostatin-14 like peptides.";		
L L	FEBS Lett. 321:279-284(1993).		
N N	[3]		
N P	SEQUENCE FROM N.A.		
X X	Kopatz S.A., Aronstam R.S., Sharma S.V.;		
T T	"cDNA clones of human proteins involved in signal transduction		
T T	sequenced by the Guthrie cDNA resource center ( <a href="http://www.cdna.org">www.cdna.org</a> ).";		
L L	Submitted [JUN-2003] to the EMBL/Genbank/DDBJ databases.		
N N	[4]		
N P	SEQUENCE FROM N.A.		
X X	MEDLINE=20057165; PubMed=10591208;		
A A	Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,		
A A	Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,		
A A	Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,		
A A	Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,		
A A	Burtill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,		
A A	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,		
A A	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,		

RA Dharni P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,  
 RA Hall R.E., Hall-Ramlyn G., Heathcote R.W., Ho S., Holmes S.,  
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,  
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,  
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Swann R.M.,  
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuoyama S.,  
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,  
 RA Fulton R., Johnson D., Benis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goela D., Graves I., Hawkins J.,  
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,  
 RA Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,  
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,  
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
 RA Edemann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
 RA Peyraud M., Kedra D., Seroussi E., Fransson I., Rapla I., Bruder C.E.,  
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
 RA Khan A.S., Lane L., Tilahun Y., Wright H.,  
 RA "The DNA sequence of human chromosome 22";  
 RL Nature 402:489-495(1999).  
 CC -!- FUNCTION: Receptor for somatostatin-14 and -28. This receptor is  
 CC coupled via pertussis toxin sensitive G proteins to inhibition of  
 CC adenylyl cyclase.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Brain, pituitary and pancreas.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL: M56738; AA60592.1; --  
 CC EMBL: 282188; CAB45263.1; --  
 CC EMBL: AY322541; AAP84354.1; --  
 CC PIR: A46226; A46226.  
 CC HSP: P34996; 1DDO.  
 CC Genbank: HGNC:11332; SSTR3.  
 CC MIM: 182453; --  
 CC GO: GO:0005887; C: integral to plasma membrane; TAS.  
 CC GO: GO:0004994; F: somatostatin receptor activity; TAS.  
 CC GO: GO:0007267; P: cell-cell signaling; TAS.  
 CC GO: GO:0007187; P: G-protein signaling, coupled to cyclic nucl. .; TAS.  
 CC GO: GO:0008628; P: induction of apoptosis by hormones; TAS.  
 CC GO: GO:0008285; P: negative regulation of cell proliferation; TAS.  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7cm1; 1.  
 CC PRINTS: PR00237; GPCR\_Rhodopsn.  
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Multigene family; Polymorphism.  
 CC DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 44 69 1 (POTENTIAL).

FT DOMAIN 70 79  
 FT TRANSMEM 80 101  
 FT DOMAIN 102 116  
 FT TRANSMEM 117 138  
 FT TRANSMEM 139 161  
 FT TRANSMEM 162 181  
 FT TRANSMEM 182 205  
 FT TRANSMEM 206 231  
 FT TRANSMEM 232 257  
 FT TRANSMEM 258 279  
 FT TRANSMEM 280 293  
 FT TRANSMEM 294 316  
 FT TRANSMEM 317 418  
 FT CARBOHYD 17 17  
 FT CARBOHYD 30 30  
 FT DISULFID 116 191  
 FT DOMAIN 346 360  
 FT VARIANT 411 411  
 FT SEQUENCE 418 AA; 45847 MW; 1227095F801190C4 CRC64;  
 SQ  
 Query Match 25.4%; Score 456.5; DB 1; Length 418;  
 Best Local Similarity 32.4%; Pred. No. 2.7e-25;  
 Matches 112; Conservative 75; Mismatches 128; Indels 31; Gaps 11;  
 QY 1 MNPFHSCWNTSALLNKS--WNKEFAVQTAS-----VVDTVILPSPMIGLICSTGLV 50  
 DB 1 MDMLPSSVSTTSEPENASSAWPPDNLGNVSAGSPAGLAVSGVLIPLVYLVVGVGLL 60  
 QY 51 GNILVFTIIR-SRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPLCTII 109  
 DB 61 GNSLIVYVVLHRTASPSVTNVILNALADELMGLPFLAAQNAL-SYWPFGSIMCRLV 119  
 QY 110 TSLDTGNCFASATMVSVDYRYALVOPFLTRWRYRTIRINLGLWASFTLALPVW 169  
 DB 120 MAVDGINOFTSIFCLTVMSVDYRYALVHPTSRKWRTPAVARTVSAWVWASVVVLPV 179  
 QY 170 VYSKVIKKGVSFCAPDLTSPDDVLM---YTLVLTITITFFPFLPLILVVCYLICXTWE 226  
 DB 180 VFSGVPR---GMSTCHMQWPEP-AAANRAGLIITVTAALGFFGLVLCVCLLVV---- 230  
 QY 227 MYQNKNDARCNPSPVKOR--VMKLTQVVLVWVVLVLSAAPHYQIVLWLOM---BQPT 281  
 DB 231 VKVRSAGRVRWAPSQCQRSSRRERRVTRMVAVVALFVLCWMPFYVLMVNVVCPBPBP- 289  
 QY 282 LAFYGVGYLISLVSASSINPFLYLLSGNFKQRLPOIQRATEX 327  
 DB 290 AFFGLYFVVALPYANSCANPILYGLFSYFKQGRFVRLRPSPR 334  
 RESULT 11  
 SSR1 HUMAN STANDARD; PRT; 391 AA.  
 ID SSR1 HUMAN 391 AA.  
 AC P30872;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Somatostatin receptor type 1 (SSIR) (SRIF-2).  
 GN SSTR1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92108031; PubMed=1346068;  
 RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;  
 RT "Cloning and functional characterization of a family of human and  
 RT mouse somatostatin receptors expressed in brain, gastrointestinal  
 RT tract, and kidney.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:251-255(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RL sequenced by the Guthrie CDNA resource center (www.cdna.org).";  
 RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RP [3]  
 RC SEQUENCE FROM N.A.  
 RD TISSUE=Brain;  
 RE MEDLINE=2238257; PubMed=12477932;  
 RF Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan E., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinska M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RL human and mouse cDNA sequences";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP [4]  
 RE INTERACTION WITH SKB1.  
 RF MEDLINE=20200451; PubMed=10734105;  
 RA Schwaerzer A., Kreienkamp H.-J., Richter D.;  
 RT "Interaction of the somatostatin receptor subtype 1 with the human  
 RL homolog of the Shk1 kinase-binding protein from yeast";  
 CC J. Biol. Chem. 275:9557-9562(2000).  
 CC -/- FUNCTION: Receptor for somatostatin with higher affinity for  
 CC somatostatin-14 than -28. This receptor is coupled via pertussis  
 CC toxin sensitive G proteins to inhibition of adenylyl cyclase. In  
 CC addition it stimulates phosphotyrosine phosphatase and Na(+)/H(+)   
 CC exchanger via pertussis toxin insensitive G proteins.  
 CC -/- SUBUNIT: Interacts with SKB1.  
 CC -/- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -/- TISSUE SPECIFICITY: Fetal kidney, fetal liver, and adult pancreas,  
 CC brain, lung, jejunum and stomach.  
 CC -/- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 CC -----  
 DR EMBL; M81829; AA58247.1; ..  
 DR EMBL; AX322536; AAF84349.1; ..  
 DR EMBL; BC035618; AAF35618.1; ..  
 DR PIR; A41795; A41795.  
 DR Genew; HGNC:11330; SSTR1.  
 DR MIM; 182451; ..  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004994; F:somatostatin receptor activity; TAS.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0007586; P:digestion; TAS.  
 DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.  
 DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.  
 DR GO; GO:0007584; P:response to nutrients; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHOPOSPN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEPT\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEPT\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Lipoprotein; Palmitate.  
 FT DOMAIN 1 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 57 84 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 85 94 2 (POTENTIAL).  
 FT TRANSMEM 95 120 3 (POTENTIAL).  
 FT DOMAIN 121 131 4 (POTENTIAL).  
 FT TRANSMEM 132 153 5 (POTENTIAL).  
 FT DOMAIN 154 175 6 (POTENTIAL).  
 FT TRANSMEM 176 196 7 (POTENTIAL).  
 FT DOMAIN 197 219 8 (POTENTIAL).  
 FT TRANSMEM 220 244 9 (POTENTIAL).  
 FT DOMAIN 245 270 10 (POTENTIAL).  
 FT TRANSMEM 271 296 11 (POTENTIAL).  
 FT DOMAIN 297 303 12 (POTENTIAL).  
 FT TRANSMEM 304 327 13 (POTENTIAL).  
 FT DOMAIN 328 391 14 (POTENTIAL).  
 FT CARBOHYD 4 44 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 44 48 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 130 208 BY SIMILARITY.  
 FT LIPID 339 S-palmitoyl cysteine (Potential).  
 SQ SEQUENCE 391 AA; 42686 MW; 85C99AFF339A43D CRC64;  
 Query Match 25.0%; Score 449; DB 1; Length 391;  
 Best Local Similarity 31.3%; Pred. No. 8.6e-25;  
 Matches 102; Conservative 67; Mismatches 111; Indels 46; Gaps 9;  
 QY 35 VILPSMIGIICSTGLVGNILVFTIIR-SRKTVPDIYICNLAVADLVHIVGMPLI--- 90  
 DB 59 ILISFIYSVCLVGLCGNSMVIYVILRYAKMKTATNIYILNLAIADELLMLSPFLVTST 118  
 QY 91 ---HQWARGGGEWFGGGLCTIITSIDTCNCFACSAIMTVMSVDYFALVQPFRLTRWETR 147  
 DB 119 LLRH-----WPGALLCRLVLSVDVAVNMETSYCLFVLSVDYFVAVVHKAARYRP 171  
 QY 148 YKTRINIGLWASFIILALPVVYSKVIFKFDGVESCAFDLTSPD--VLAYTLYLTITT 205  
 DB 172 TVAKVNLGVWVLSLVLPVWFSRTAANSDDGTACNMLMPEPAQRWLGVFLYTFMG 231  
 QY 206 FPFPLPLVLCYIILCYT-----WEMVQONKDKACCNPSPKQKVMKLTSMVLV 257  
 DB 232 FLLPVGALCLCYLIIAQRVWALKAGNQ--QRKRSR-----KITLVWVVV 277  
 QY 258 VVFTLSAAPHYIQLVNLQEQPTLAFVGYLYSLICLSYASSINPELYILLGNFKRL 317  
 DB 278 MVFVICWMPFVQVNVVFAEQDDATV---SLSVLGYANSCANPILYGLFLSDNFKRSF 334  
 QY 318 PQI-----ORRATEKEINNMGNLTLS 338  
 DB 335 QRILCLSMWMDNAEPPVDYATALKS 360  
 RESULT 12  
 SSTR1\_MOUSE  
 ID SSTR1\_MOUSE STANDARD; PRT; 391 AA.  
 AC P30873;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Somatostatin receptor type 1 (SSIR) (SRIF-2).  
 GN SSTR1 OR SSTR1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92108031; PubMed=1346068;  
 RA Yamada Y., Post S.R., Wang K., Tager H.S., Bell G.I., Seino S.;  
 RT "Cloning and functional characterization of a family of human and  
 RT mouse somatostatin receptors expressed in brain, gastrointestinal  
 RT tract, and kidney.";









SSR3\_RAT STANDARD; PRT; 428 AA.  
P30936;  
01-JUL-1993 (Rel. 26, Created)  
01-JUL-1993 (Rel. 26, Last sequence update)  
10-OCT-2003 (Rel. 42, Last annotation update)  
DE Somatostatin receptor type 3 (SS3R) (SSR-28).  
GN SSTR3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
SEQUENCE FROM N.A.  
RP STRAIN=Wistar; TISSUE=Brain;  
RC MDLINE=93066220; PubMed=1279674;  
RX Meyerhof W., Wulfsen I., Schoenrock C., Fehr S., Richter D.;  
RA "Molecular cloning of a somatostatin-28 receptor and comparison of  
RT its expression pattern with that of a somatostatin-14 receptor in rat  
RT brain";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:10267-10271(1992).  
CC -!- FUNCTION: Receptor for somatostatins-14 and -28. This receptor is  
CC coupled via pertussis toxin sensitive G proteins to inhibition of  
CC adenylyl cyclase.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Densely expressed in cerebellum and in  
CC moderate levels in the amygdala, cortex, striatum, spleen, liver,  
CC pituitary.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X63574; CAA45130.1; -  
CC PIR; S30508; S30508.  
CC HSSP; P34996; 1DDD.  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm1.1.  
CC PRINTS; PR00237; GPCRHOPOFSN.  
CC PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1;  
CC PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
KW G-protein coupled receptor; transmembrane; Glycoprotein;  
KW Multigene family.  
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 46 71 1 (POTENTIAL).  
FT DOMAIN 72 81 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 82 103 2 (POTENTIAL).  
FT DOMAIN 104 118 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 119 140 3 (POTENTIAL).  
FT DOMAIN 141 162 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 163 182 4 (POTENTIAL).  
FT DOMAIN 183 206 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 207 232 5 (POTENTIAL).  
FT DOMAIN 233 266 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 267 288 6 (POTENTIAL).  
FT DOMAIN 289 302 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 303 325 7 (POTENTIAL).  
FT DOMAIN 326 428 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DISULFID 117 192 BY SIMILARITY.  
FT DOMAIN 358 373 POLY-GLU.  
SQ SEQUENCE 428 AA; 47151 MW; BE0AA948940A9E9D CRC64;

Search completed: May 13, 2004, 16:18:56  
Job time : 19 secs

Query Match 24.6%; Score 441.5; DB 1; Length 428;  
Best Local Similarity 31.8%; Pred. No. 3.1e-24;  
Matches 108; Conservative 73; Mismatches 136; Indels 23; Gaps 10;  
QY 1 MNPFHA-SCWNTSAELLKSNKEFAYQTASVVDVILPSMIGICSTGLVGNILIVFTI 59

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2004, 16:15:11 ; Search time 45 Seconds  
(without alignments)  
2383.915 Million cell updates/sec

Title: US-09-913-770B-1  
Perfect score: 1798  
Sequence: 1 MPPFASCWNTSAELLKSW.....QRRATEKINNMTLKSHF 340

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_podent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1648	91.7	340	6 Q8MIN7	Q8min7 mustela put
2	1577	87.7	330	6 Q8MIP5	Q8mip5 canis faml
3	571.5	31.8	331	13 Q801F3	Q801f3 figu rubrip
4	569.5	31.7	354	11 Q8X3M8	Q8x3m8 mus musculu
5	568	31.6	360	13 Q801F2	Q801f2 figu rubrip
6	566.5	31.5	353	6 Q8MIP6	Q8mip6 canis faml
7	565.5	31.5	353	6 Q8MIN8	Q8min8 mustela put
8	551.5	30.7	328	13 Q801F5	Q801f5 brachydanio
9	548.5	30.5	322	13 Q801F6	Q801f6 brachydanio
10	484.5	26.9	377	13 Q7T2S9	Q7t2s9 carassius a
11	468.5	26.1	330	13 Q8GQ4	Q8gq4 carassius a
12	467.5	26.0	350	13 Q9DGQ6	Q9dgq6 carassius a
13	467.5	26.0	452	13 Q7T2S8	Q7t2s8 carassius a
14	464	25.8	370	13 Q8UWL5	Q8uwl5 figu rubrip
15	458.5	25.5	385	11 Q9JK40	Q9jk40 mus musculu
16	456.5	25.4	385	4 Q86YF2	Q86yf2 homo sapien

17	455.5	25.3	367	6 Q8MI04	Q8mi04 ovis aries
18	451	25.1	346	6 Q95KS6	Q95ks6 ovis aries
19	449.5	25.0	367	13 Q9PVF9	Q9pvf9 carassius a
20	447	24.9	367	13 Q9PVG0	Q9pvgo carassius a
21	446	24.8	390	13 Q8AXM7	Q8axm7 carassius a
22	440.5	24.5	390	11 Q7T86	Q7t86 rattus norv
23	423.5	23.6	315	6 Q9GKP7	Q9gkp7 sus scrofa
24	421	23.4	385	11 Q8BQ97	Q8bq97 mus musculu
25	421	23.4	477	13 Q8JID5	Q8jid5 carassius a
26	406	22.6	370	13 Q7T068	Q7t068 rana pipien
27	404.5	22.5	366	4 Q8IWP3	Q8iwp3 homo sapien
28	400.5	22.3	377	13 Q8U14	Q8u14 brachydanio
29	393.5	21.9	438	11 Q8CAN5	Q8can5 mus musculu
30	392	21.8	388	13 Q7T069	Q7t069 rana pipien
31	390	21.7	388	11 Q8CH75	Q8ch75 mus musculu
32	390	21.7	390	11 Q8V171	Q8v171 mus musculu
33	390	21.7	391	11 Q8V170	Q8v170 mus musculu
34	390	21.7	392	11 Q8CH74	Q8ch74 mus musculu
35	390	21.7	393	11 Q8R1M0	Q8r1m0 mus musculu
36	390	21.7	401	11 Q9R1L9	Q9r1l9 mus musculu
37	390	21.7	409	11 Q8V169	Q8v169 mus musculu
38	390	21.7	425	11 Q8CH73	Q8ch73 mus musculu
39	390	21.7	438	11 Q9R0D1	Q9r0d1 mus musculu
40	390	21.7	444	11 Q9J1Y1	Q9j1y1 mus musculu
41	390	21.7	456	11 Q8CGW2	Q8cgw2 mus musculu
42	388	21.6	400	11 Q8CGM4	Q8cgm4 cavia porce
43	388	21.6	418	4 Q8IWN3	Q8iwn3 homo sapien
44	388	21.6	446	4 Q8IWN4	Q8iwn4 homo sapien
45	388	21.6	454	4 Q9H573	Q9h573 homo sapien

#### ALIGNMENTS

#### RESULT 1

Q8MIN7 PRELIMINARY; PRT; 340 AA.

AC Q8MIN7; DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Melanin-concentrating hormone receptor subtype 2 MCH-2R.  
OS Mustela putorius (European polecat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
OC Mustela.  
OX NCBI\_TaxID=9668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,  
RA Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,  
RA Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,  
RA Van der Ploeg L.H.T., Howard A.D.,  
RT "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species-Specific Gene Expression."  
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RL EMBL, AY112899; AAM51633.1;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR008362; MCH2\_receptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PRINTS; PR01784; MCH2RECEPTOR.  
DR PRINTS; PR01783; MCHRECEPTOR.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 340 AA; 38889 MW; E0F0BF65B8157A6C CRC64;

Query Match	91.7%	Score 1648;	DB 6;	Length 340;																																																						
Best Local Similarity	91.2%;	Pred. No. 1.5e-146;																																																								
Matches 310;	Conservative 14;	Mismatches 16;	Indels 0;	Gaps 0;																																																						
Qy	1	MNP	PHAS	CWNTS	SAEL	LKSN	KFA	Q	TAS	V	D	T	V	I	P	S	M	I	G	I	C	S	T	G	L	V	G	N	I	L	V	F	T	I	60																							
Ddb	1	MNS	LH	SCWNTS	SAEL	LKSN	KSN	E	S	A	Q	T	U	R	I	V	D	T	I	L	F	S	M	I	G	I	C	S	M	G	L	V	G	N	I	L	V	F	T	I	60																	
Qy	61	RSR	KKT	V	P	D	I	Y	I	C	N	L	A	V	A	D	I	H	V	G	M	P	F	L	I	H	O	W	A	R	G	G	E	W	F	G	G	P	L	C	T	I	I	S	L	D	T	C	N	O	F	A	C	120				
Ddb	61	RSR	K	T	P	D	I	Y	I	C	N	L	A	V	A	D	I	H	V	G	M	P	F	L	I	H	O	W	A	R	G	G	E	W	F	G	G	P	L	C	T	I	I	S	L	D	T	C	N	O	F	A	C	120				
Qy	121	S	A	I	M	T	V	N	S	V	D	R	Y	F	A	L	V	O	P	F	R	L	T	R	W	R	T	R	Y	K	T	I	R	I	N	L	G	L	W	A	S	F	I	A	L	P	W	Y	T	S	K	V	I	K	E	D	G	180
Ddb	121	S	A	I	M	T	V	N	S	V	D	R	Y	F	A	L	V	O	P	F	R	L	T	R	W	R	T	R	Y	K	T	I	R	I	N	L	G	L	W	A	S	F	I	A	L	P	W	Y	T	S	K	V	I	K	E	D	G	180
Qy	181	V	E	S	C	A	F	L	T	S	P	D	D	V	L	T	Y	L	T	I	T	T	F	F	F	P	L	P	I	L	V	C	I	L	I	L	C	Y	T	W	E	M	Y	Q	N	K	D	A	R	C	N	P	S	240				
Ddb	181	V	E	S	C	A	F	L	T	S	P	D	D	V	L	T	Y	L	T	I	T	T	F	F	F	P	L	P	I	L	V	C	I	L	I	L	C	Y	T	W	E	M	Y	Q	N	K	D	A	R	C	N	P	S	240				
Qy	241	V	P	K	O	R	V	M	K	L	T	R	W	L	V	L	V	V	F	I	S	A	A	P	H	V	I	Q	L	V	N	L	Q	M	E	O	P	T	L	A	F	V	G	V	I	S	I	C	L	S	Y	A	S	S	300			
Ddb	241	V	P	K	E	R	V	M	K	L	T	R	W	L	V	A	V	F	I	S	A	A	P	H	V	I	Q	L	V	N	L	Q	M	E	O	P	T	L	A	F	V	G	V	I	S	I	C	L	S	Y	A	S	S	300				
Qy	301	I	N	P	F	L	Y	I	L	L	S	N	G	K	R	L	P	O	I	O	R	E	A	T	E	K	E	I	N	N	M	G	N	T	L	K	S	H	F	340																		
Ddb	301	I	N	P	F	L	Y	I	L	S	N	G	K	R	L	P	O	I	O	R	E	A	T	E	K	E	I	N	N	M	G	N	T	L	K	S	H	F	340																			
Qy	301	I	N	P	F	L	Y	I	L	S	N	G	K	R	L	P	O	I	O	R	E	A	T	E	K	E	I	N	N	M	G	N	T	L	K	S	H	F	340																			
Ddb	301	I	N	P	F	L	Y	I	L	S	N	G	K	R	L	P	O	I	O	R	E	A	T	E	K	E	I	N	N	M	G	N	T	L	K	S	H	F	340																			
Qy	301	I	N	P	F	L	Y	I	L	S	N	G	K	R	L	P	O	I	O	R	E	A	T	E	K	E	I	N	N	M	G	N	T	L	K	S	H	F	340																			
Ddb	301																																																									

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1  MYSLHSSCWNTSAEPLANKSCNEKPAYHTLSILDTKRLPSMIGLICSMGLVGNILVFTII 60
61  RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGGPELCTIIITSLDTCNQFAC 120
61  RSRKKTIPDIYICNLAVADLVHICMPFLIHQWARGGEWFGGPELCTIIITSLDTCNQFAC 120
121  SAKTVMVSVDVRPVALVQPPRLFRWTRVKTIRINLGLWAASFILALPVWYYSKVIFKDG 180
121  SAKTVMVSIDRYALVQPELTSWTRVKTIRINLGLWAASFILALPVWYYSKVIFKDG 180
181  VESCAFDLTSPDDVLWYTLITITTFPPPLPLINVCYIILCYTWEMYQONKQDARCNPS 240
181  VESCAFDLTSPDDVLRYTYLITITTFPPPLPLINVCYIILCYTWEMYQONKQDARCNPS 240
241  VPKQRVMKLTQWVLNVAVVVFLISAAPYHVIQVNLQMBOPTLAPVVGXYLSICLSVASS 300
241  VPKERVNKLTKWVLNVAUVFLISAAPYHVIQVNLQMBQOPTLAPVVGXYLSICFSVASS 300
301  INPFLYILSGNFQKELPQIQORATEK 327
301  INPFLYILSGNFQKELPQVQRRVTEK 327

RESULT 3
Q801F3 PRELIMINARY; PRT; 331 AA.
AC Q801F3;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Melanin-concentrating hormone receptor 1 (Fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxId=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,
RA Currie P.D., Jackson I.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161860; AAC24755.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . ; IEA.
DR GO; GO:0004872; F:melanin-concentrating hormone receptor activity; IEA.
DR GO; GO:0001594; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004047; MCH1_receptor.
DR InterPro; IPR008361; MCH_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR0237; GPCR_RHODOPSN.
DR PRINTS; PR01507; MCH1RECEPTOR.
DR PRINTS; PR01783; MCHRECEPTOR.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 331 AA; 36947 MW; 532D0D9C4B74AD1D CRC64;

Query Match 31.8%; Score 571.5; DB 13; Length 331;
Best Local Similarity 39.8%; Pred. No. 2e-45;
Matches 123; Conservative 60; Mismatches 107; Indels 19; Gaps 7;

QY 36 ILPSMIGLICSTGLVGNILVFTIR-----RKKTVPDIYICNLAVADLVHIVGMPFLIH 91
DB 2 VLPVIFGICLLGLGVANSAAVITYVQTKCHKAKQIVDPDIFILNSVDLLFLGLGMPFLIH 61
QY 92 QWARGGGEWFGGPELCTIIITSLDTCNQFACSAITVMVSVDVRPVALVQPELFRWTRVKT 150
DB 62 QLLGNSTWHFGGVCYVITALDSNSOIVSTYLLTAMTLDRLYATVHPFRFIRTPRVAT 121

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QY 151 IRINLGLWAASFILALPVWYYSKVIKFDGVSACFDLTSP--DVLWYTLTYITTFPP 209
Db 122 LVIGL-VWGMSTIIPVWYAGLWPLDGSVACALLPNVSDTYWTLTQFFLAFALP 180
QY 210 LPLILVCYLILCYTWYQQNDARCCNPSVPKQ---RVMKLTQVLLVWVVFILSAAP 266
Db 181 LAVICLVFPKIL-----QMSASVA-PLPERSLRVTRKVRMAVMICLAFPICWAP 231
QY 267 YHVIVOLVNLQEOPTLAFVGVYLSICLSYASSINPFLYLLSGNFQKRLPQIORRATE 326
Db 232 YVVLQVLHVGQNPALAFSAYNIAISMGYANSCINPFLYIMQSETFRKQLLRAVRPVHR 291
QY 327 KEINMGNT 335
Db 292 KVRNPSIT 300

RESULT 4
Q8K3M8 PRELIMINARY; PRT; 354 AA.
AC Q8K3M8
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Melanin-concentrating hormone receptor 1 alternate form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Lakaye B., Adamantidis A., Coumans B., Zorzi W., Parmentier M.,
RA Grisar T.;
RT "Cloning of the mouse melanin-concentrating hormone receptor 1 gene
RT and promoter characterization.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY049011; AAL06070.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0030273; F:melanin-concentrating hormone receptor acti. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004047; MCH1_receptor.
DR InterPro; IPR008361; MCH1_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01507; MCH1RECEPTOR.
DR PRINTS; PR01783; MCHRECEPTOR.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 354 AA; 39380 MW; C8088113F93619A5 CRC64;

Query Match 31.7%; Score 569.5; DB 11; Length 354;
Best Local Similarity 36.7%; Pred. No. 3.3e-45;
Matches 114; Conservative 60; Mismatches 114; Indels 23; Gaps 4;

QY 35 VILPSMIGIICSTGLVGNILIVFTIIRSK-----KIVPDIVICNLAVADLVHVGMPFLI 90
Db 42 IIMPSVFGITCLGIVGNSTVFAVVKSKLHWCNSVDPFIINLSVVDLLFLLGMPFI 101
QY 91 HQWARGGEVFGPCTIITSLDTCNCFACSAIMTVMSVDYFALVQPFRLTRWTRYKT 150
Db 102 HQMGNGVWHFGEITCTILTAMANDANSQFTSTYILTAMADRYLATVHFISSTKPKPSMA 161
QY 151 IRINLGLWAASFILALPVWYYSKVIKFDGVSACFDLTSP--DVLWYTLTYITTFPP 209
Db 162 TLVICLLWALSISITPWLYARLIPFGGAVCGGIRLPNPDYDLNLTLYQFFLAFALP 221
QY 210 LPLILVCYLILCYTWYQQNDARCCNPSVP-----KORVMKLTQVLLVWVVFILS 263
Db 222 FVVIITAAVYKIL-----QRMTSSVAPASQSRIRLTKEVTRTAICLVFVFC 269

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QY 264 AAPYHVIVOLVNLQEOPTLAFVGVYLSICLSYASSINPFLYLLSGNFQKRLPQIORR 323
Db 270 WAPYVVLQQLTQLSISRPTLTFVLYINAAISLGYANSCINPFLYIVLCETPRKRLVLSVKP 329
QY 324 ATEKEINMGNT 334
Db 330 AAQQLRTVSN 340

RESULT 5
Q801F2 PRELIMINARY; PRT; 360 AA.
ID Q801F2
AC Q801F2
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Melanin-concentrating hormone receptor 2.
GN MCHR2.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
SEQUENCE FROM N.A.
RA Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,
RA Currie P.D., Jackson I.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161861; AAO24756.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR008361; MCH1_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01783; MCHRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 360 AA; 40871 MW; CD97C3DB3AFC1BB CRC64;

Query Match 31.6%; Score 568; DB 13; Length 360;
Best Local Similarity 39.4%; Pred. No. 4.7e-45;
Matches 112; Conservative 64; Mismatches 94; Indels 14; Gaps 4;

QY 36 ILPSMIGIICSTGLVGNILIVFTIIRSKKTVPDIYICNLAVADLVHVGMPFLIHQWAR 95
Db 40 IFPTIYGLCSGVGIANGLVYIAYTVCKKQWSDIYVLNLAIDMLFLVWPNHQLVR 99
QY 96 GGEWVFGPCLTITSLDTCNCFACSAIMTVMSVDYFALVQPFRLTRWTRYKTIRINL 155
Db 100 DROWVGFNFCMAVVVDVSNQFTVGIVTCLIDRYALVHP--TSERTIQWTLIINM 157
QY 156 GLWAASFILALPVWYYSKVIKFDGVSACFDLTSPDDVLYWYLYITTTFFPFLPLIV 215
Db 158 LVWLGSELLTPVWLYAKV-EQRQNTFVCMNLDGDPEDMYWYLYQSILGFIPLIIST 216
QY 216 CYTILLCYTWYQQNDARCCNPSVPKQSV--MKLTQVLLVWVVFILSAAPVHVITLV 273
Db 217 FYSLTLYHVFSSIRRVK-----RKQSWARRATKQVLMVIGLFCWSYHVITQVL 267
QY 274 NLQEOPTLAFVGVYLSICLSYASSINPFLYLLSGNFQKRL 317
Db 268 NISNHNPTVSVYAYXINISICLSYSHSCINPLMLLIFAQNYRRL 311

RESULT 6
Q8MIP6 PRELIMINARY; PRT; 353 AA.
ID Q8MIP6

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AC QBMIP6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Melanin-concentrating hormone receptor subtype 1.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,  
RA Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,  
RA Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,  
RA Van der Ploeg L.H.T., Howard A.D.;  
RT "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species  
RT Specific Gene Expression";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY112858; AAM51851.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR004047; MCH1\_receptor.  
DR InterPro; IPR008361; MCH\_receptor.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCRHHODOPS.  
DR PRINTS; PR01507; MCH1RECEPTOR.  
DR PRINTS; PR01783; MCHRECEPTOR.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 353 AA; 39064 MW; 3D8FC5FAF047A93B CRC64;  
Query Match 31.5%; Score 566.5; DB 6; Length 353;  
Best Local Similarity 37.0%; Pred. No. 6.3e-45;  
Matches 113; Conservative 62; Mismatches 119; Indels 11; Gaps 4;  
QY 35 VILPSMIGICSTGLVGNILVFTIIRSK----KTVPIYICNLAVADLVHVGMPFLI 90  
DB 41 IIMPSVFGTICLLGIIGNSTVPAVVKSKLHWCSNVDPDIINLSVVDLLFLGMPFI 100  
QY 91 HOWARGEVWFGPLCTIITSLDTCNQFACSAIMTVSVSDRYFALVQPFRLTRWTRYKT 150  
DB 101 HQLMGNGVWHFGETMCTLTAMDANSQFTSYLTAMADRYLATVHPISSTFKRPSVA 160  
QY 151 IRINLGLWAASFTIALPVWVYKVKFDGVESCAFDELTSPP-DVLWYLYLTITTFPPF 209  
DB 161 TLVICLLWALSFSITPVWLYARLIPFGGTGCGIRLPNDTDLWYFTLYOFFLAFALP 220  
QY 210 LPILVCYIILCYTWEMVQONKARCCNPSPVKQRMVSKLTKMWLVVVVFTLSAAPHV 269  
DB 221 FVVIITAYVRIL-----QRMSSVAPASORSIRLTKRVTRTAICLVFVWCAPYIV 274  
QY 270 IQLVNLQMEQPTLAFYVGYVLSICLSYASSINPFYILLSGNFQKRLPQIORRATEREI 329  
DB 275 LQTLQSLISSEPTLTFVLYNNAISLGANSCLNPFVIVLCETFRKELVLSVKPAAQGL 334  
QY 330 NNMGN 334  
DB 335 RAVSN 339  
RESULT 7  
QBMIN8 PRELIMINARY; PRT; 353 AA.  
AC QBMIN8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Melanin-concentrating hormone receptor subtype 1 MCH-1R.  
OS Mustela putorius (European polecat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
OC Mustela.  
OX NCBI\_TaxID=9668;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tan C.P., Sano H., Iwaasa H., Pan J., Sailer A., Hreniuk D.L.,  
RA Feighner S.D., Palyha O.C., Figueroa D.J., Austin C.P., Jiang M.M.,  
RA Yu H., Ito J., Ito M., Ito M., Guan X.M., Kanatani A.,  
RA Van der Ploeg L.H.T., Howard A.D.;  
RT "Melanin-Concentrating Hormone Receptor Subtypes 1 and 2: Species  
RT Specific Gene Expression";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY112898; AAM51632.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0030273; F:melanin-concentrating hormone receptor acti. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR004047; MCH1\_receptor.  
DR InterPro; IPR008361; MCH\_receptor.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCRHHODOPS.  
DR PRINTS; PR01507; MCH1RECEPTOR.  
DR PRINTS; PR01783; MCHRECEPTOR.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 353 AA; 38935 MW; 4A489B97EAC85D76 CRC64;  
Query Match 31.5%; Score 565.5; DB 6; Length 353;  
Best Local Similarity 36.3%; Pred. No. 7.8e-45;  
Matches 113; Conservative 61; Mismatches 114; Indels 23; Gaps 4;  
QY 35 VILPSMIGICSTGLVGNILVFTIIRSK----KTVPIYICNLAVADLVHVGMPFLI 90  
DB 41 IIMPSVFGTICLLGIIGNSTVPAVVKSKLHWCSNVDPDIINLSVVDLLFLGMPFI 100  
QY 91 HOWARGEVWFGPLCTIITSLDTCNQFACSAIMTVSVSDRYFALVQPFRLTRWTRYKT 150  
DB 101 HQLMGNGVWHFGETMCTLTAMDANSQFTSYLTAMADRYLATVHPISSTFKRPSVA 160  
QY 151 IRINLGLWAASFTIALPVWVYKVKFDGVESCAFDELTSPP-DVLWYLYLTITTFPPF 209  
DB 161 TLVICLLWALSFSITPVWLYARLIPFGGTGCGIRLPNDTDLWYFTLYOFFLAFALP 220  
QY 210 LPILVCYIILCYTWEMVQONKARCCNPSPVKQRMVSKLTKMWLVVVVFTLS 263  
DB 221 FVVIITAYVRIL-----QRMSSVAPASORSIRLTKRVTRTAICLVFVVC 268  
QY 264 AAPVHVITQLVNLQMEQPTLAFYVGYVLSICLSYASSINPFYILLSGNFQKRLPQIORR 323  
DB 269 WAPYIVLQTLQSLISSEPTLTFVLYNNAISLGANSCLNPFVIVLCETFRKELVLSVKP 328  
QY 324 ATEKEINMGN 334  
DB 329 AAQGLRAISN 339  
RESULT 8  
QBMIF5 PRELIMINARY; PRT; 328 AA.  
AC QBMIF5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Melanin-concentrating hormone receptor 1b (Fragment).  
GN MCH1B.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;

[1] SEQUENCE FROM N.A.  
RP Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,  
RA Currie P.D., Jackson I.J.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY161858; AAC24753.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0030273; F:melanin-concentrating hormone receptor acti...; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007218; P:pineuropeptide signaling pathway; IEA.  
DR InterPro; IPRO00276; GPCR Rhodpsn.  
DR InterPro; IPRO00306; IG\_MHC.  
DR InterPro; IPRO04047; MCH1\_receptor.  
DR InterPro; IPRO08361; MCH1\_Receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PRINTS; PR01507; MCHRECEPTOR.  
DR PRINTS; PR01783; MCHRECEPTOR.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Receptor.  
FT NON\_TER  
SQ SEQUENCE 328 AA; 36702 MW; 1B41A65641EDAD0F CRC64;

Query Match 30.7%; Score 551.5; DB 13; Length 328;  
Best Local Similarity 37.1%; Pred.No. 1.5e-43;  
Matches 108; Conservative 66; Mismatches 98; Indels 19; Gaps 5;

QY 35 VILPSMIGIICSTGLVGNLIIVFTIIRSK---KTVDDIYCINLAVALDVHVGMPLII 90  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 VLMPISGVICFYGIIGNCIVIYTKTKFAQAQTVPDIFFISLCIALDLFLGMLPII 60  
QY 91 HOWARGGEWVGSGPLCTITSLDTCNQFACSAIMTWSVDRYFALVQPFLRNTRYKT 150  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 61 DLQVGNGFCFGTMCTVTITELDSNRNINSTILTWTLDRLVATVHFNFHTPRVA 120

QY 151 IRNLGLWAASFILALPVWMYSVKIFKDGVESCAFDLTSP-DDVLWTLTYLTITTFPPF 209  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 121 VAUVLVWLISLSITSIPVMNYAGLMPLRDGSMGCALLPNPATDYTWETLYQVFALA 180

QY 210 LPILVCYLILCYTEMWYOQNKKARCCNPSPKQ-----RVMKLTRKLVLVVVFI 265  
Db 181 LVTCVVFVKIL-----QNNAAVTA--PLIQSLRVRTPKVRMAVICIAFFICWA 230

QY 266 PYHVIQLVNQMEOPTLAFVGYVYLSICLSYASSINSPLYILLSGNQFR 316  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 231 PHYLQLAHLVSQRSPSFVLFAYNVAINSYANSCINPLLMISETFRQ 281

RESULT 9  
QS01F6 PRELIMINARY; PRT; 322 AA.  
ID Q801F6 AC Q801F6  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Melanin-concentrating hormone receptor la (fragment).  
GN MCHRIA.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
[1]  
SEQUENCE FROM N.A.  
RP Logan D.W., Bryson-Richardson R.J., Pagan K.E., Taylor M.S.,  
RA Currie P.D., Jackson I.J.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY161857; AAC24752.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0030273; F:melanin-concentrating hormone receptor acti...; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007218; P:pineuropeptide signaling pathway; IEA.  
DR InterPro; IPRO00276; GPCR Rhodpsn.  
DR InterPro; IPRO00306; IG\_MHC.  
DR InterPro; IPRO04047; MCH1\_receptor.  
DR InterPro; IPRO08361; MCH1\_Receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRRHODOPSN.  
DR PRINTS; PR01507; MCHRECEPTOR.  
DR PRINTS; PR01783; MCHRECEPTOR.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Receptor.  
FT NON\_TER  
SQ SEQUENCE 322 AA; 35831 MW; D041EBE8941B004E CRC64;

Query Match 30.5%; Score 548.5; DB 13; Length 322;  
Best Local Similarity 37.6%; Pred.No. 2.8e-43;  
Matches 109; Conservative 65; Mismatches 97; Indels 19; Gaps 4;

QY 36 ILPSMTIGIICSTGLVGNLIIVFTIIR----SRKKTVPDIYCINLAVALDVHVGMPLII 91  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 2 ILPSIFGIICFLGISNSIWVTTIKTKCKAQAKTPDIFINFNISVIDLLFLLGMPFLII 61

QY 92 QWARGGEWVGSGPLCTITSLDTCNQFACSAIMTWSVDRYFALVQPFLRNTRYKT 151  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 62 QLINGSGWCFGATMCKVISALDNSQTSYSTILTWTLDRLVATVHFNFHNRTCVAS 121

QY 152 RINLGLWAASFILALPVWMYSVKIFKDGVESCAFDLTSPD-DVLWTLTYLTITTFPP 210  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 122 AVVAATAALSISTIPVMNYTGMLPHSGOVGCCALLPNPSTNICWFIIYQVLAFA 181

QY 211 PLILVCYLILCYTEMWYOQNKKARCCNPSPKQ-----RVMKLTRKLVLVVVFI 266  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 182 TIICVVFVKIL-----KHMSITVAPLRPNQQVTRKSVTRMAVICIAFFICWA 231

QY 267 YHVIQLVNQMEOPTLAFVGYVYLSICLSYASSINSPLYILLSGNQFR 316  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 232 YYLQILVHLGIQKPSASFYVTHVAISMGYANSCLNPFYIILLSKTFRQ 281

RESULT 10  
Q7T2S9 PRELIMINARY; PRT; 377 AA.  
ID Q7T2S9 AC Q7T2S9  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Somatostatin receptor type five subtype C.  
GN SST5C.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
[1]  
SEQUENCE FROM N.A.  
RP MEDLINE=22465070; PubMed=12576085;  
RA Lin X., Peter R.E.;  
RT "Somatostatin-like receptors in goldfish: cloning of four new  
   receptors";  
RL Peptides 24:53-63(2003).  
DR EMBL; AF472593; AAP68899.1; -.  
KW Receptor.  
SQ SEQUENCE 377 AA; 41898 MW; FBFOCF0F022AB148 CRC64;

Query Match 26.9%; Score 484.5; DB 13; Length 377;  
Best Local Similarity 36.8%; Pred.No. 3.4e-37;  
Matches 113; Conservative 64; Mismatches 107; Indels 23; Gaps 10;

QY 21 NKLEFAYOTASVDVTIPLSPMIGICTGLVGNLIIVFTIIR-SRKKTVPDIYCINLA 79  
Dy :|::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 39 DSMFPQGSSWTAVISFTFVIV---GLGTNTLAIVYVRVAKMKTVTNIYILNA 95

QY 80 LHVIGVMPFLIHQWARGGEWVGSGPLCTITSLDTCNQFACSAIMTWSVDRYFALV 139

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Db 96 ELVINGLPFLTTQNL-SYWPFGSLCRVVTADSLNQFTSFCLTVMGIDRYLAVVHPI 154
QY 140 RLTRWTRYKTIINLGLWAASLILPVMVYSKVIKFDGVESCAFDLTSPDDVLWYTL 199
Db 155 RSTKWRPRVAKAVSAVAFAFVFLVPIVSDV---QDTFNCNMSWPEPRDI-WSTA 210
QY 200 YLTIT---FFFLPPLILVCYIILCVTWEMYQONKDACRNCNPSVPKOR--VMKLTVMYL 254
Db 211 FLYATLGFGLPLVICMCLLIV-----VKVSSGARA---GPTKRRSERKVTMVV 262
QY 255 VLWVVFILSAAPHVLIQVLNQLQWEOPTLAFYVG-YVLSICLSYASSINPFYILLSGNF 313
Db 263 VVVVFLWCLWPLFYIINVLNLPENSVMAGVYFFAVILSYANSCANPLLYGLSDNF 322
QY 314 QKRLPOI 320
Db 323 QKSRKV 329

RESULT 11
Q8QGO4
ID Q8QGO4 PRELIMINARY; PRT; 390 AA.
AC Q8QGO4;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Type five-like somatostatin receptor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Peter R.E.;
RT "Cloning and expression of a type five-like somatostatin receptor in
goldfish".
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF252879; AAM18805.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECF1_1; 1.
DR PROSITE; PS00242; G-PROTEIN_RECF1_2; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 390 AA; 44136 MW; EC12119A4B6CF9A8 CRC64;

Query Match 26.1%; Score 468.5; DB 13; Length 390;
Best Local Similarity 36.7%; Pred. No. 1.1e-35;
Matches 120; Conservative 60; Mismatches 122; Indels 25; Gaps 12;

QY 7 SCWNTS-AELLNKS--WNKEFAQTASV-----DTVLPSMIGIICSTGLGNILIVFTI 59
Db 6 SMCNTSISDYANGSNEFNTHQLNGSSMAEEDSTKILAVILVPPVVGILTGNLSAIFV 65
QY 60 IR-SRKTVDPDIYICNLAVDLVHVMPL-IHQWARGGEVFGGFLCTIITSLDTCNQ 117
Db 66 LRYTKMTATNATNILLNLADEYIIGLFLTAHML--GYWFGNLCRLWNTDSISQ 123
QY 118 FACSALMTVMSVDYFALVQPFRLTRWTRYKTIINLGLWAASLILPVMVYSKVIK 177
Db 124 FTSTFCLTMSIDRYMAVHPISARWRPRVAKVINSMWALSCLLTLPVIYCDV--- 180
QY 178 KDGVESCAFDLTSPDDVLWY---LYLTITTFPPLILVCYIILCVTWEMYQONKDA 234

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Db 181 QPELNTCNLSWPERDV-WSTAFILYATMLGFFPLMVICLXLLIV-----IKVKSASA 234
QY 235 RCCNPSVPKQVWMLTKWLVLVVVFILSAAPHVLIQVLNQLQWEOPTLAFYVG-YVLSIC 293
Db 235 R-AGLSKRGREKVKTRVRIIVVVVFLWCLWPLFYIINLNLSTLPENSIMTGIYFLTVI 293
QY 294 LSYASSINPFYILLSGNFQKRLPOI 320
Db 294 LTYVNSCANPLLYSFLSDNFKRSFQV 320

RESULT 12
Q9DGO6
ID Q9DGO6 PRELIMINARY; PRT; 380 AA.
AC Q9DGO6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Somatostatin receptor type two.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
RT "Molecular cloning and expression of a type-two somatostatin receptor
in goldfish brain and pituitary.".
RL Mol. Cell. Endocrinol. 166:75-87 (2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF139597; AAF98367.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECF1_1; 1.
DR PROSITE; PS00242; G-PROTEIN_RECF1_2; 1.
DR PROSITE; PS00242; G-PROTEIN_RECF1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 380 AA; 43146 MW; CE897FF7537CFA30 CRC84;

Query Match 26.0%; Score 467.5; DB 13; Length 380;
Best Local Similarity 33.1%; Pred. No. 1.4e-35;
Matches 111; Conservative 69; Mismatches 114; Indels 41; Gaps 10;

QY 27 QTASVDTVLPSMIGIICSTGLGNILIVFTIIR-SRKTVDPDIYICNLAVDLVHVI 85
Db 48 QTSWVITFV---YFVVCVAGLCGNALVMYVILRYAKMKVTNIVILNLAADVLCMLS 103
QY 86 MPF-----LIHQWARGGEVFGGFLCTIITSLDTCNQFACSAIMTWMSVDYFALVQPF 139
Db 104 LPFATQISLH-----WPFGSAICRVLTADSMNQFTSIFLTVMSFDRYLAVVHPI 156
QY 140 RLTRWTRYKTIINLGLWAASLILPVMVYSKVIKFDGVESCAFDLTSPDDVLWYTL 199
Db 157 KSTKWRPRMAKSISLAWVILNLPIMYSGVNVKNKNEARTKMLWPEPQNT-YTV 215
QY 200 YLTIT---TFPPLILVCYIILCVTWEMYQONKDACRNCNPSVPKORVMKLTVMYL 256
Db 216 FIFTFMGFLPLVICMCLLIV-----IKVSSGMVCS--SKKRSERKVTMVV 269
QY 257 VVVFILSAAPHVLIQVLNQLQWEOPTLAFYVGYY-LSTCLSYASSINPFYILLSGNFQK 315
Db 270 VVVFVCLWCLWPLFYIINVLNLPENSVMAGVYFFAVILSYANSCANPLLYAFLSDNF 329

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QY 316 R-----LPOIQRATEKEINNMGNLTLS 338
Db 330 SFQVNLCKRVGGLDEIERSQDRTRVNDVMS 364

RESULT 13
Q7T2S8
ID Q7T2S8 PRELIMINARY; PRT; 452 AA.
AC Q7T2S8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Type-three somatostatin receptor subtype B.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN SEQUENCE FROM N.A.
RP MEDLINE=22465070; PubMed=12576085;
RX Lin X., Peter R.E.; receptors in goldfish: cloning of four new
RT "Somatostatin-like receptors in goldfish: cloning of four new
RL Peptides 24:53-63 (2003).
DR EMBL; AF510109; AAP68900.1; -.
KW Receptor.
SQ SEQUENCE 452 AA; 50776 MW; DBA53D223D5B16D8 CRC64;

Query Match 26.0%; Score 467.5; DB 13; Length 452;
Best Local Similarity 32.6%; Pred. No. 1.6e-35;
Matches 113; Conservative 81; Mismatches 116; Indels 37; Gaps 14;

QY 6 ASCW-NTSAEL-NKSNKEFAYQTASVVDV-----VILPSMIGIICSTGLVGN 52
Db 15 APVWNTASSMTPNQFPFPPYLOTEINTDSTLDYAPGAVGILPLIYIVVINGLIGN 74

QY 53 ILIVFTIIR-SRKKTVPDIYICNLAVDLVHIVGMPFLIHQWARGG--EWVFGPLCTII 109
Db 75 TLVHIVLAYSQAESVTNIYILNLAIDLEFLGLPFLAVQ---NGLLSWPFGLMCLRLV 131

QY 110 TSLDTCNQFACSAITMNSVDVFEALVQPFRLTRKTYKTIIRNLGLWAASFIILAPFW 169
Db 132 MTVDAINQTSITFCITVMSIDRYLAVHPLQSRWRQPRVAKMVAATVNGISFVVLPFW 191

QY 170 VYSKVIKFDGVESCAFDLTSPDDVLW---YLYLTITITFFPFLPLILVCYLILCYLTYWE 226
Db 192 VFAGVLQ-DG--NCSIVWPEAEV-WKATFIVYATVGFPGFLAVICLCYLLIV----- 242

QY 227 MTQONKDKARCCNPSVPKQR-VKLTWNLVLVWVFLSNAAPHVQLVNLQWQPTLAFY 285
Db 243 VKVRSGRVRATSIIRRKSECKITRMVVIVVAVFVCLWLPFYVLNIVNLVLVLPF-DFR 301

QY 286 VGYLSICLSYASSINPELYILLSGN----FOKRLPQIQRATEKE 328
Db 302 GLYFYVVLVSANCANPLYGLSDNFKRGFKALCRSRVENVQD 348

RESULT 14
Q8UWL5
ID Q8UWL5 PRELIMINARY; PRT; 370 AA.
AC Q8UWL5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Somatostatin receptor 2.
GN SSTR2.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;

[1]
SEQUENCE FROM N.A.
MEDLINE=21564205; PubMed=11707075;
RA Bagheri-Fam S., Ferraz C., Demaille J., Scherer G., Pfeifer D.;
RT "Comparative Genomics of the SOX9 Region in Human and Fugu rubripes:
RT Conservation of Short Regulatory Sequence Elements within Large
RT Intergenic Regions.";
RL Genomics 78:73-82 (2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF329945; AAL32173.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 370 AA; 41364 MW; 420BB12F204946B6 CRC64;

Query Match 25.8%; Score 464; DB 13; Length 370;
Best Local Similarity 33.1%; Pred. No. 2.8e-35;
Matches 108; Conservative 64; Mismatches 114; Indels 40; Gaps 9;

QY 5 HASCWNTSAELLNKNMKNKEFAYQTASVVDVTPILPSMIGIICSTGLVGNILIVFTIIR-SR 63
Db 31 HA---NRFDHSLNKT-----STVITCMYFLVCAVGLCGNALVIYVILRYAK 74

QY 64 KKTVPDIYICNLAVDLVHIVGMPFLIHQWARGGEVFGPLCTIITSLDTCNQFACSAI 123
Db 75 MKVTNIIYILNLAVDVLEMLGLPFLAIQLAL-VHWPFGVLCRVVMTVDSLNQFTSIFC 133

QY 124 MTWNSVDVRYALVQPFRLTRKTYKTIIRNLGLWAASEFTILAPVWVYSKVIKFDGVES 183
Db 134 LMNSIDRYLAVHPLQSRWRQPRVAKTINAVWGLASLVNLPFIVYISGIIITKQDCG-F 192

QY 184 CAFDLTSPDDVLW---YLYLTITITFFPFLPLILVCYLILCYLTYWVYQONKDKARCCNPSV 241
Db 193 CTIVWPEEAEYATFMIYTFILGFLPLDLVLSLCYVFII-----VKVKSIGIRVGSSK 246

QY 242 PKQRVKLTWNLVLVWVFLSNAAPHVQLVNL-----QMEQPTLAFVGYLSICL 294
Db 247 RKSERKVTWNSIVVAVFVCLWLPFYVFNVTSGISATHVLRSTFAFW-----VL 300

QY 295 SYASSINPELYILLSGNFQKRLPQI 320
Db 301 GYANSCANPLYAFLENFKKSFQNV 326

RESULT 15
Q9JK40
ID Q9JK40 PRELIMINARY; PRT; 385 AA.
AC Q9JK40;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Somatostatin subtype 5 receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=129/SV;
RC O'Carroll A.-M.;
RA "Cloning, sequence and tissue distribution of the gene encoding a
RT mouse somatostatin subtype 5 receptor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

```



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OM protein - protein search, using sw model

Run on: May 13, 2004, 16:08:21 ; Search time 58 Seconds  
(without alignments)  
1636.313 Million cell updates/sec

Title: US-09-913-770B-1

Perfect score: 1798

Sequence: 1 MNPFPASCWNTSAGLLNKS.....QRRATEKINNMGNTLKSHF 340

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1798	100.0	340	3 AAB23540	AAB23540 Human G-p
2	1798	100.0	340	4 AAU25610	AAU25610 Human G-p
3	1798	100.0	340	4 AAB68428	AAB68428 Amino aci
4	1798	100.0	340	4 AAU51567	AAU51567 Human mel
5	1798	100.0	340	4 AAB68893	AAB68893 Human AXO
6	1798	100.0	340	4 AAU04381	AAU04381 Human G-p
7	1798	100.0	340	5 AAU77532	AAU77532 G protein
8	1798	100.0	340	5 AAU97733	AAU97733 Human TGR
9	1798	100.0	340	6 AAE311492	AAE311492 Human MCH
10	1798	100.0	340	6 AAE114795	AAE114795 Human mel
11	1798	100.0	340	6 AAE35562	AAE35562 Human mel
12	1798	100.0	340	6 AAQ27467	AAQ27467 Human mel
13	1798	100.0	340	7 ABW00463	ABW00463 Human G-p
14	1793	99.7	340	5 ABQ7996	ABQ7996 Human sev
15	1792	99.7	340	6 ABP81746	ABP81746 Human G-p
16	1785	98.2	340	7 ABW01467	ABW01467 Monkey MC
17	1764	98.1	340	7 ADE24736	ADE24736 Monkey me
18	1763	98.1	340	6 AAE311491	AAE311491 Rhesus mo
19	1760	97.9	340	4 AAU51568	AAU51568 Human mel
20	1755	97.6	340	7 ABW01468	ABW01468 Monkey MC
21	1754	97.6	335	5 AAE18650	AAE18650 Human G-p
22	1699	93.9	340	6 AAE311490	AAE311490 Ferret MC
23	1644	91.4	340	7 ADE24746	ADE24746 Cat melan
24	1588	88.3	330	7 ABW01469	ABW01469 Canine MC
25	1588	88.3	330	7 ADE24756	ADE24756 Dog melan

26	1581	87.9	330	6 AAE31489	AAE31489 Dog MCH-2
27	843	46.9	318	7 ADC12692	ADC12692 Human GPC
28	747.5	41.6	347	7 ABW01478	ABW01478 Monkey MC
29	744.5	41.4	359	7 ABW01474	ABW01474 Monkey MC
30	736	40.9	352	7 ABW01473	ABW01473 Monkey MC
31	670.5	37.3	345	7 ABW01475	ABW01475 Monkey MC
32	569.5	31.7	353	3 AAB13437	AAB13437 Rat MCH1
33	569.5	31.7	353	3 AAB12778	AAB12778 Rat SLC-1
34	569.5	31.7	353	3 AAU97310	AAU97310 Murine 11
35	569.5	31.7	353	3 AAB96870	AAB96870 Rat SLC-1
36	569.5	31.7	353	4 AAB85896	AAB85896 Mouse MCH
37	569.5	31.7	353	4 AAB81124	AAB81124 Rat melan
38	569.5	31.7	353	4 AAB48152	AAB48152 Rat melan
39	569.5	31.7	353	5 AAG80610	AAG80610 Rat SLC-1
40	569.5	31.7	353	5 ABB04940	ABB04940 Rat SLC-1
41	569.5	31.7	353	5 AAU75854	AAU75854 Rat melan
42	569.5	31.7	353	5 AAU77540	AAU77540 Melanin c
43	569.5	31.7	353	5 AAU76894	AAU76894 Rat melan
44	569.5	31.7	353	6 ADA45226	ADA45226 Rat SLC-1
45	569.5	31.7	353	6 ABR58246	ABR58246 Rat melan

## ALIGNMENTS

RESULT 1  
AAB23540  
ID AAB23540 standard; protein; 340 AA.  
XX  
AC AAB23540;  
XX  
DT 02-JAN-2001 (first entry)  
XX  
DE Human G-protein coupled receptor SLT protein sequence.  
XX  
KW G-protein coupled receptor; SLT; antiallergic; antirheumatic;  
KW antidiabetic; norepinephrine; neuroprotective; antiinflammatory; neuroleptic;  
KW hypotensive; nervous system disorder; hormonal disorder; schizophrenia;  
KW inflammatory diseases; cardiovascular disease; Alzheimer's disease;  
KW allergy; rheumatism; sodium intolerance; diabetes; hypertension.  
XX  
OS Homo sapiens.  
XX  
FN WO200049046-A1.  
XX  
PD 24-AUG-2000.  
XX  
PF 18-FEB-2000; 2000WO-JP000927.  
XX  
PR 19-FEB-1999; 99JP-00041336.  
PR 06-MAY-1999; 99JP-00125768.  
XX  
(TAKE ) TAKEDA CHEM IND LTD.  
XX  
Watanabe T, Terao Y, Shintani Y;  
XX  
WPI; 2000-543749/49.  
XX  
N-PSDB; AAA90097.

G protein coupled receptor protein SLT, DNA encoding it and antibodies recognizing it, useful for treatment and diagnosis of e.g. neurological diseases.  
Claim 1; Fig 1; 108pp; Japanese.  
This invention relates to a G-protein coupled receptor protein, SLT of human origin. The nucleotide and protein sequences are given in the specification. The invention includes expression vector containing SLT encoding polynucleotide sequences, host cells transformed with the vectors, and methods for preparing SLT through the culturing of the transformants. Also included are anti-SLT antibodies, SLT ligands and methods for their identification. SLT exhibits antiallergic, antirheumatic, antidiabetic, norepinephrine, neuroprotective,

CC antiinflammatory, neuroleptic, and hypotensive activity. The G protein  
CC coupled receptor protein SLT, the DNA encoding it and its antibodies can  
CC be used for the diagnosis and treatment of diseases with which SLT is  
CC associated, such as disorders of SLT expression. These include nervous  
CC system disorders, hormonal disorders, inflammatory diseases,  
CC cardiovascular diseases, and liver/gall bladder/pancreas diseases (such  
CC as Alzheimer's disease, schizophrenia, allergies, rheumatism, sodium  
CC intolerance, diabetes and hypertension). The present sequence represents  
CC the SLT protein sequence of the invention  
XX  
SQ Sequence 340 AA;  
  
Query Match 100.0%; Score 1798; DB 3; Length 340;  
Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNPFCSCWNTSABLKNKSNKEFAYQTASVVDVILPMSMIGIICSTGLVGNILIVFTII 60  
DB 1 MNPFCSCWNTSABLKNKSNKEFAYQTASVVDVILPMSMIGIICSTGLVGNILIVFTII 60  
QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGFLCTIITSLDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGFLCTIITSLDTCNQFAC 120  
QY 121 SAIMTVMSVDYRYFALVQFFRLTRWRTYKTIIRINLGLWAASFILALPVWYYSKVIKFDG 180  
DB 121 SAIMTVMSVDYRYFALVQFFRLTRWRTYKTIIRINLGLWAASFILALPVWYYSKVIKFDG 180  
QY 181 VESCAFDLTSPDDVILVTLTITITFFFPFLILVLCVTLVWYQVYVYVYVYVYVYVYVYV 240  
DB 181 VESCAFDLTSPDDVILVTLTITITFFFPFLILVLCVTLVWYQVYVYVYVYVYVYVYVYV 240  
QY 241 VPKQVVKMLTKQVILVWVVFILSAAPYHVITQVNLQWQPTLAFYVYVYVYVYVYVYVYVYV 300  
DB 241 VPKQVVKMLTKQVILVWVVFILSAAPYHVITQVNLQWQPTLAFYVYVYVYVYVYVYVYVYV 300  
QY 301 INPFLYILLSGNFQKRLPQIORRATEKEINNMGNLTLSKSHF 340  
DB 301 INPFLYILLSGNFQKRLPQIORRATEKEINNMGNLTLSKSHF 340  
  
RESULT 2  
AAU25610  
ID AAU25610 standard; protein; 340 AA.  
XX  
AC AAU25610;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #57..  
XX  
KW Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;  
KW attention deficit disorder; anxiety; depression; bipolar disorder;  
KW neurological disorder; Huntington's disease; dementia; obesity; anorexia;  
KW metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;  
KW type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;  
KW cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;  
KW viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;  
KW antidepressant; anorectic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO200162797-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-US005676.  
XX  
PR 23-FEB-2000; 2000US-0184247P.  
PR 23-FEB-2000; 2000US-0184303P.  
PR 23-FEB-2000; 2000US-0184304P.  
PR 23-FEB-2000; 2000US-0184305P.  
PR 23-FEB-2000; 2000US-0184306P.  
PR 23-FEB-2000; 2000US-0184307P.

PR 02-MAR-2000; 2000US-0186457P.  
PR 03-MAR-2000; 2000US-0186810P.  
PR 09-MAR-2000; 2000US-0188064P.  
PR 13-MAR-2000; 2000US-0188808P.  
PR 13-MAR-2000; 2000US-0194344P.  
PR 23-JUN-2000; 2000US-0213861P.  
PR 11-JUL-2000; 2000US-0217369P.  
PR 11-JUL-2000; 2000US-0217370P.  
PR 14-JUL-2000; 2000US-0218337P.  
PR 20-JUL-2000; 2000US-0218492P.  
XX  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
PA Vogeli G, Wood LS, Parodi LA, Lind P;  
PI WPI; 2001-570628/64.  
XX N-PSDB; AAS42862.  
DR  
XX New isolated nucleic acid encoding a new G-protein coupled receptor  
PT polypeptide for detecting receptor modulators that can treat mental  
PT disorders, such as schizophrenia, anxiety, depression, or obesity.  
XX  
XX Claim 35; Page 93; 279pp; English.  
XX  
XX Sequences AAU25554-AAU25616 represent human G-protein coupled receptor  
CC (GPCR) polypeptides of the invention. The proteins and their associated  
CC DNA sequences can be used to identify compounds which bind to GPCR  
CC polypeptides and in screening for compounds that modulate GPCR activity.  
CC By screening a human subject for the presence of mutations in GPCR DNA, a  
CC GPCR-related disorder or a genetic predisposition can be diagnosed. The  
CC sequences can also be used for treatment and prevention of mental  
CC disorders such as schizophrenia, attention deficit disorder, anxiety,  
CC depression, dementia and bipolar disorder, neurological disorders such as  
CC Huntington's disease, Parkinson's disease and Tourette's syndrome,  
CC metabolic disorders such as obesity, anorexia and type 2 diabetes,  
CC cardiovascular disorders such as thrombosis, myocardial infarction,  
CC cardiomyopathy and atherosclerosis, viral infections caused by HIV and  
CC cancers  
XX  
SQ Sequence 340 AA;  
  
Query Match 100.0%; Score 1798; DB 4; Length 340;  
Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNPFCSCWNTSABLKNKSNKEFAYQTASVVDVILPMSMIGIICSTGLVGNILIVFTII 60  
DB 1 MNPFCSCWNTSABLKNKSNKEFAYQTASVVDVILPMSMIGIICSTGLVGNILIVFTII 60  
QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGFLCTIITSLDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVFGGFLCTIITSLDTCNQFAC 120  
QY 121 SAIMTVMSVDYRYFALVQFFRLTRWRTYKTIIRINLGLWAASFILALPVWYYSKVIKFDG 180  
DB 121 SAIMTVMSVDYRYFALVQFFRLTRWRTYKTIIRINLGLWAASFILALPVWYYSKVIKFDG 180  
QY 181 VESCAFDLTSPDDVILVTLTITITFFFPFLILVLCVTLVWYQVYVYVYVYVYVYVYVYV 240  
DB 181 VESCAFDLTSPDDVILVTLTITITFFFPFLILVLCVTLVWYQVYVYVYVYVYVYVYVYV 240  
QY 241 VPKQVVKMLTKQVILVWVVFILSAAPYHVITQVNLQWQPTLAFYVYVYVYVYVYVYVYVYV 300  
DB 241 VPKQVVKMLTKQVILVWVVFILSAAPYHVITQVNLQWQPTLAFYVYVYVYVYVYVYVYVYV 300  
QY 301 INPFLYILLSGNFQKRLPQIORRATEKEINNMGNLTLSKSHF 340  
DB 301 INPFLYILLSGNFQKRLPQIORRATEKEINNMGNLTLSKSHF 340  
  
RESULT 3  
AAB68428  
ID AAB68428 standard; protein; 340 AA.

XX AAB68428;  
 XX AC  
 XX DT 23-JUL-2001 (first entry)  
 XX DE Amino acid sequence of human G-protein coupled receptor HG67.  
 XX KW G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress;  
 XX KW melanin concentrating hormone receptor; cancer; pain; sexual dysfunction;  
 XX KW weight gain; hypertension; dyslipidemia; cardiovascular disease;  
 XX KW gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;  
 XX KW cachexia.  
 XX OS Homo sapiens.  
 XX PN WO200136479-A1.  
 XX DT 25-MAY-2001.  
 XX DE 14-NOV-2000; 2000WO-US031240.  
 XX PF 16-NOV-1999; 99US-0165871P.  
 XX PR 13-MAR-2000; 2000US-0188977P.  
 XX PR 18-APR-2000; 2000US-0198029P.  
 XX PA (MERI ) MERCK & CO INC.  
 XX PA (BANY ) BANYU PHARM CO LTD.  
 XX PI Liu Q, McDonald TP, Howard AD, Iwaasa H, Sano H;  
 XX PI WPI; 2001-355618/37.  
 XX DR N-PSDB; AAF85372.  
 XX DR  
 XX PT New G-protein coupled receptor, designated MCH-R2, is a receptor for  
 XX PT melanin-concentrating hormone and is useful to provide treatment for  
 XX PT weight disorders including obesity.  
 XX PS Claim 4; Page 25; 32pp; English.  
 XX CC The present sequence represents a human G-protein coupled receptor,  
 XX CC designated HG67 or MCH-R2. HG67 is a melanin concentrating hormone  
 XX CC receptor. Modulators of HG67 can be used to treat a patient, particularly  
 XX CC to reduce weight, particularly in obesity, or to treat stress. These  
 XX CC modulators can also be used to treat cancer, reduce pain, treat sexual  
 XX CC dysfunction or to produce weight gain. Bringing about weight loss can be  
 XX CC used to reduce the likelihood of hypertension, diabetes, dyslipidemia,  
 XX CC cardiovascular disease, gall stones, osteoarthritis or certain forms of  
 XX CC cancers. Increasing weight can be useful in the treatment of anorexia,  
 XX CC AIDS, wasting, cachexia and frail elderly patients, or those undergoing  
 XX CC chemotherapy or radiation therapy  
 XX SQ Sequence 340 AA;  
 Query Match 100.0%; Score 1798; DB 4; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPFFASCWNTSAELLNKSNNKEFAYQTASVVDVTLPSMIGIICSTGLVGNILIVFTII 60  
 DB 1 MNPFFASCWNTSAELLNKSNNKEFAYQTASVVDVTLPSMIGIICSTGLVGNILIVFTII 60  
 QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120  
 DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120  
 QY 121 SAINTVMSVDRYFALVQPFELTRWRTRKYKTIRINLGLWAASFILALPVWYVKVFKFDG 180  
 DB 121 SAINTVMSVDRYFALVQPFELTRWRTRKYKTIRINLGLWAASFILALPVWYVKVFKFDG 180  
 QY 181 VESCAFDLTSPDDVWLYTLTITTTFFPLPLVLCYILLCYTWMYQNKDARCCNS 240  
 DB 181 VESCAFDLTSPDDVWLYTLTITTTFFPLPLVLCYILLCYTWMYQNKDARCCNS 240

QY 241 VPKQRVMKLTQWLVLVVVVILSAAPYHVIQLVNLQMEQPTLAFYVGYLSYASSS 300  
 DB 241 VPKQRVMKLTQWLVLVVVVILSAAPYHVIQLVNLQMEQPTLAFYVGYLSYASSS 300  
 QY 301 INPELYILLSGNFOKRLPOIORRATERKEINNMGNLTAKSHF 340  
 DB 301 INPELYILLSGNFOKRLPOIORRATERKEINNMGNLTAKSHF 340  
 RESULT 4  
 AAMS1567  
 ID AAMS1567 standard; protein; 340 AA.  
 XX AAMS1567;  
 XX AC  
 XX DT 16-JAN-2002 (first entry)  
 XX DE Human melanin concentrating hormone receptor #1.  
 XX KW Human; melanin concentrating hormone; MCH; MCH receptor;  
 XX KW G protein coupled receptor; obesity; cachexia; anorexia nervosa;  
 XX KW hyperphagia; anorectic; anti-anorectic.  
 XX OS Homo sapiens.  
 XX PN WO200170975-A1.  
 XX DT 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-JP002343.  
 XX PR 24-MAR-2000; 2000JP-00088588.  
 XX PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 XX PA (HELI-) HELIX RES INST.  
 XX PI Kurama T, Matsumoto S, Takasaki J, Matsumoto M, Kamohara M;  
 XX PI Saito T, Oda T, Saito Y;  
 XX DR WPI; 2001-639126/73.  
 XX DR N-PSDB; AAI71927.  
 XX PT New protein with melanin concentrating hormone receptor activity, for  
 XX PT finding antagonists for treating obesity and eating disorders.  
 XX PS Claim 1; Page 48-50; 62pp; Japanese.  
 XX CC The invention relates to a novel protein comprising a fully defined 340  
 XX CC amino acid sequence, or the sequence containing one or more amino acid  
 XX CC substitutions, deletions or insertions. The protein shows melanin  
 XX CC concentrating hormone (MCH) receptor activity. It is a G protein coupled  
 XX CC receptor that binds to MCH. The protein is used to find agents to treat  
 XX CC obesity, cachexia, anorexia nervosa and hyperphagia. The present sequence  
 XX CC is a human MCH receptor polypeptide of the invention  
 XX SQ Sequence 340 AA;  
 Query Match 100.0%; Score 1798; DB 4; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPFFASCWNTSAELLNKSNNKEFAYQTASVVDVTLPSMIGIICSTGLVGNILIVFTII 60  
 DB 1 MNPFFASCWNTSAELLNKSNNKEFAYQTASVVDVTLPSMIGIICSTGLVGNILIVFTII 60  
 QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120  
 DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120  
 QY 121 SAINTVMSVDRYFALVQPFELTRWRTRKYKTIRINLGLWAASFILALPVWYVKVFKFDG 180  
 DB 121 SAINTVMSVDRYFALVQPFELTRWRTRKYKTIRINLGLWAASFILALPVWYVKVFKFDG 180

QY 181 VESCAFDTSPDDVLTWLTLYLTITTTFFPLPLILVCYVILLCYTWMYQONKDKARCCNPS 240  
 DB 181 VESCAFDTSPDDVLTWLTLYLTITTTFFPLPLILVCYVILLCYTWMYQONKDKARCCNPS 240  
 QY 241 VPQRVMKLTWLVLVVVVILSAAPYHVIQVNLQMEQPTLAFYGYYSICLSYASSS 300  
 DB 241 VPQRVMKLTWLVLVVVVILSAAPYHVIQVNLQMEQPTLAFYGYYSICLSYASSS 300  
 QY 301 INPFLYILLSGNFQRLPQIQRATEKEINNMGNTLKS HF 340  
 DB 301 INPFLYILLSGNFQRLPQIQRATEKEINNMGNTLKS HF 340

RESULT 5  
 AAB68893  
 ID AAB68893 standard; protein; 340 AA.  
 AC AAB68893;  
 DT 24-APR-2001 (first entry)  
 DE Human AXOR21.  
 KW Human; AXOR21; G-protein coupled receptor; anorectic; antidiabetic;  
 KW cytotatic; antiasthmatic; antiparkinsonian; cardiac; hypertensive;  
 KW osteopathic; antianginal; cerebroprotective; antitumor; antiallergic;  
 KW antimigraine; anesthetic; tranquiliser; antimanic; gene therapy; vaccine;  
 KW cancer; neurological disorder.  
 OS Homo sapiens.  
 XX WO200107606-A1.  
 EN 01-FEB-2001.  
 PD 27-JUL-2000; 2000WO-GB002899.  
 PF 27-JUL-1999; 99GB-00017627.  
 PR 24-AUG-1999; 99GB-00020046.  
 XX (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA Duckworth DM, Hill J, Muir AI, Szekeres PG;  
 PI WPI: 2001-182790/18.  
 XX N-PSDB; AAF58619.  
 DR Novel G-protein coupled receptor polypeptide, AXOR21, useful for treating  
 XX obesity, diabetes, eating disorders such as anorexia and bulimia,  
 PT hypertension, osteoporosis, angina pectoris and myocardial infarction.  
 PS Claim 1; Page 31; 42pp; English.  
 CC The present sequence is AXOR21, a G-protein coupled receptor. AXOR21  
 CC polynucleotides and polypeptides are useful for treating and diagnosing  
 CC conditions such as pain, cancers, diabetes, obesity, anorexia, bulimia,  
 CC asthma, Parkinson's disease, acute heart failure, hypotension,  
 CC hypertension, urinary retention, osteoporosis, angina pectoris,  
 CC myocardial infarction, stroke, ulcers, allergies, benign prostatic  
 CC hypertrophy, migraine, vomiting, psychotic and neurological disorders  
 CC including anxiety, schizophrenia, manic depression, depression, delirium,  
 CC dementia and severe mental retardation, and dyskinesia such as  
 CC Huntington's disease or Gilles de la Tourette's syndrome. AXOR21  
 CC polynucleotides and polypeptides are also useful for screening and  
 CC structure based designing of antagonists, agonists and inhibitors of  
 CC AXOR1. AXOR21 polynucleotides are useful for chromosome localisation  
 CC studies, as diagnostic reagents for detecting mutations in associated  
 CC genes, and as valuable tools for tissue expression studies. AXOR21  
 CC polynucleotides and polypeptides are useful as vaccines  
 XX Sequence 340 AA;  
 SQ Query Match 100.0%; Score 1798; DB 4; Length 340;

Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPHASCNWTSABELLNKSNKEPAYQTASVVDVTILPMSMIGIICSTGLVGNILIVFTII 60  
 DB 1 MNPHASCNWTSABELLNKSNKEPAYQTASVVDVTILPMSMIGIICSTGLVGNILIVFTII 60  
 QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVGGPLCTIITSLDTCNPFAC 120  
 DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWVGGPLCTIITSLDTCNPFAC 120  
 QY 121 SAIMTVMSVDYRFALVQPFRLTRWTRTKTIRINLGLWAASFILALPVMYVKVIFKDG 180  
 DB 121 SAIMTVMSVDYRFALVQPFRLTRWTRTKTIRINLGLWAASFILALPVMYVKVIFKDG 180  
 QY 181 VESCAFDTSPDDVLTWLTLYLTITTTFFPLPLILVCYVILLCYTWMYQONKDKARCCNPS 240  
 DB 181 VESCAFDTSPDDVLTWLTLYLTITTTFFPLPLILVCYVILLCYTWMYQONKDKARCCNPS 240  
 QY 241 VPQRVMKLTWLVLVVVVILSAAPYHVIQVNLQMEQPTLAFYGYYSICLSYASSS 300  
 DB 241 VPQRVMKLTWLVLVVVVILSAAPYHVIQVNLQMEQPTLAFYGYYSICLSYASSS 300  
 QY 301 INPFLYILLSGNFQRLPQIQRATEKEINNMGNTLKS HF 340  
 DB 301 INPFLYILLSGNFQRLPQIQRATEKEINNMGNTLKS HF 340

RESULT 6  
 AAU04381  
 ID AAU04381 standard; protein; 340 AA.  
 AC AAU04381;  
 DT 23-OCT-2001 (first entry)  
 DE Human G-protein coupled receptor, hrUP27.  
 KW Human; G-protein coupled receptor; GPCR; hrUP27; agonist;  
 KW inverse agonist; lung cancer.  
 OS Homo sapiens.  
 XX WO200136471-A2.  
 XX 25-MAY-2001.  
 PD 16-NOV-2000; 2000WO-US031509.  
 PF 17-NOV-1999; 99US-0166088P.  
 PR 17-NOV-1999; 99US-0166099P.  
 PR 17-NOV-1999; 99US-0166369P.  
 PR 23-DEC-1999; 99US-0171900P.  
 PR 23-DEC-1999; 99US-0171901P.  
 PR 23-DEC-1999; 99US-0171902P.  
 PR 14-FEB-2000; 2000US-0181743P.  
 PR 14-MAR-2000; 2000US-0189258P.  
 PR 10-APR-2000; 2000US-0195898P.  
 PR 10-APR-2000; 2000US-0195899P.  
 PR 10-APR-2000; 2000US-0196078P.  
 PR 28-APR-2000; 2000US-0200419P.  
 PR 12-MAY-2000; 2000US-0203630P.  
 PR 12-JUN-2000; 2000US-0210741P.  
 PR 21-AUG-2000; 2000US-0226760P.  
 PR 21-AUG-2000; 2000US-0226760P.  
 PR 26-SEP-2000; 2000US-0235418P.  
 PR 26-SEP-2000; 2000US-0235779P.  
 PR 20-OCT-2000; 2000US-0242332P.  
 PR 20-OCT-2000; 2000US-0242343P.  
 PR 24-OCT-2000; 2000US-0243019P.  
 XX (AREN-) ARENA PHARM INC.

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XX  Chen R, Dang HT, Lowitz KP;
XX  WPI; 2001-355616/37.
XX  DR N-PSDB; AAS07954.
XX  Endogenous and non-endogenous versions of human G-protein coupled
XX  receptors for direct identification of candidate compounds as agonists,
XX  inverse agonists or partial agonists for use as therapeutic agents.
XX  Claim 77; Page 125-126; 160pp; English.
XX  The sequence represents a human G-protein coupled receptor (GPCR),
XX  hRUP27. The endogenous and non-endogenous, constitutively activated
XX  versions of human G-protein coupled receptors (GPCR), are useful for
XX  direct identification of candidate compounds as receptor agonists,
XX  inverse agonists or partial agonists having applicability as therapeutic
XX  agents for treating diseases related to GPCR, e.g. lung cancer. Non-
XX  endogenous version of human GPCRs are also utilized in research settings
XX  and in vitro and in vivo system, incorporating GPCRs can be utilized to
XX  elucidate and understand the roles these receptors play in the human
XX  condition, both normal and diseased
XX  SQ Sequence 340 AA;
    Query Match 100.0%; Score 1798; DB 4; Length 340;
    Best Local Similarity 100.0%; Pred. No. 5.3e-196;
    Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 MNPFFHASCWNTSAELLNKSNNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
    DB 1 MNPFFHASCWNTSAELLNKSNNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
    QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLHGWARGGEWVFGPLCTIITSIDTCNQFAC 120
    DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLHGWARGGEWVFGPLCTIITSIDTCNQFAC 120
    QY 121 SAIMTVMVDYFALVQPFRLTRNRTRYKTIRINLGLWAASFILALPVWVYSKVIKFXDG 180
    DB 121 SAIMTVMVDYFALVQPFRLTRNRTRYKTIRINLGLWAASFILALPVWVYSKVIKFXDG 180
    QY 181 VESCAFDLTSPDDVLTWYLTITITFFPFLPLILVLCYILCYTWEMVQONKDACCCNPS 240
    DB 181 VESCAFDLTSPDDVLTWYLTITITFFPFLPLILVLCYILCYTWEMVQONKDACCCNPS 240
    QY 241 VPKQRVMKLTQWLVLVVWVFLSAAPYHVIQLVNLQMEQTLAFYVGYLSICLSYASSS 300
    DB 241 VPKQRVMKLTQWLVLVVWVFLSAAPYHVIQLVNLQMEQTLAFYVGYLSICLSYASSS 300
    QY 301 INPFLYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340
    DB 301 INPFLYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340
    RESULT 7
    AAU77532
    ID AAU77532 standard; protein; 340 AA.
    AC AAU77532;
    DT 05-JUN-2002 (first entry)
    XX G protein-coupled orphan receptor protein SLT.
    XX G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;
    XX MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
    XX exogenous obesity; hyperinsular obesity; sexual function disorder;
    XX overpowering intermittent pain; still born; uterus rupture;
    XX premature birth; Prader-Willi syndrome.
    XX Homo sapiens.
    OS
    XX
    XX WO200203070-A1.
    PN

XX  10-JAN-2002.
XX  04-JUL-2001; 2001WO-JP005809.
XX  05-JUL-2000; 2000JP-00208254.
XX  (TAKE ) TAKEDA CHEM IND LTD.
XX  Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX  WPI; 2002-164552/21.
XX  DR N-PSDB; ABK10848, ABK10852.
XX  Screening for compounds or salts which alter affinity of melanin-
XX  concentrating hormone with its receptor to provide agonists as appetite-
XX  stimulating agents and its antagonist for preventing or treating obesity,
XX  uses a protein or hormone.
XX  Claim 1; Fig 1; 112pp; Japanese.
XX  The invention describes a method of screening for compounds or their
XX  salts that can change affinity of melanin-concentrating hormone (MCH)
XX  with its G protein-coupled orphan receptor protein, SLT. The screened MCH
XX  receptor agonists are useful as appetite-stimulating agents and its
XX  antagonist for preventing or treating obesity e.g. malignant
XX  mastocytosis, exogenous obesity and hyperinsular obesity, and also for
XX  treating sexual function disorders, overpowering intermittent pains,
XX  still borns, uterus rupture, premature birth and Prader-Willi syndrome.
XX  This is the amino acid sequence of the G protein-coupled orphan receptor
XX  protein, SLT
XX  SQ Sequence 340 AA;
    Query Match 100.0%; Score 1798; DB 5; Length 340;
    Best Local Similarity 100.0%; Pred. No. 5.3e-196;
    Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 MNPFFHASCWNTSAELLNKSNNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
    DB 1 MNPFFHASCWNTSAELLNKSNNKEFAYQTASVVDTVILPSMIGIICSTGLVGNILIVFTII 60
    QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLHGWARGGEWVFGPLCTIITSIDTCNQFAC 120
    DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLHGWARGGEWVFGPLCTIITSIDTCNQFAC 120
    QY 121 SAIMTVMVDYFALVQPFRLTRNRTRYKTIRINLGLWAASFILALPVWVYSKVIKFXDG 180
    DB 121 SAIMTVMVDYFALVQPFRLTRNRTRYKTIRINLGLWAASFILALPVWVYSKVIKFXDG 180
    QY 181 VESCAFDLTSPDDVLTWYLTITITFFPFLPLILVLCYILCYTWEMVQONKDACCCNPS 240
    DB 181 VESCAFDLTSPDDVLTWYLTITITFFPFLPLILVLCYILCYTWEMVQONKDACCCNPS 240
    QY 241 VPKQRVMKLTQWLVLVVWVFLSAAPYHVIQLVNLQMEQTLAFYVGYLSICLSYASSS 300
    DB 241 VPKQRVMKLTQWLVLVVWVFLSAAPYHVIQLVNLQMEQTLAFYVGYLSICLSYASSS 300
    QY 301 INPFLYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340
    DB 301 INPFLYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340
    RESULT 8
    AAU97733
    ID AAU97733 standard; protein; 340 AA.
    AC AAU97733;
    DT 27-AUG-2002 (first entry)
    XX Human TGR342 polypeptide.
    XX

```

KW Human; TGR342; receptor; G-protein coupled receptor; GPCR; TGR;  
 KW TGR-associated disorder; signal transduction; renal failure; nephritis;  
 KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;  
 KW diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;  
 KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;  
 KW circadian rhythm.

XX Homo sapiens.

XX OS  
 XX WO200242458-A2.

XX PD  
 XX 30-MAY-2002.

XX XX  
 XX 21-NOV-2001; 2001WO-US043404.

XX PR  
 XX 22-NOV-2000; 2000US-0252841P.

XX PR  
 XX 22-DEC-2000; 2000US-0257636P.

XX PR  
 XX 12-JAN-2001; 2001US-0261377P.

XX PR  
 XX 28-MAR-2001; 2001US-0279554P.

XX PR  
 XX 29-MAR-2001; 2001US-0280696P.

XX PA  
 XX (TULA-) TULARIK INC.

XX PI  
 XX Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;

XX DR  
 XX WPI; 2002-463633/49.

XX DR  
 XX N-PSDB; ABK86285.

XX FT  
 XX New isolated G-protein couple receptor polypeptide, termed TGR, for

XX FT  
 XX diagnosis and treatment of diseases such as renal failure, nephritis,

XX FT  
 XX hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.

XX PS  
 XX Claim 33; Page 73; 98pp; English.

XX CC  
 XX The invention relates to a G-protein coupled receptor polypeptide (GPCR),  
 CC termed TGR, and its associated nucleic acid. The sequences of the  
 CC invention are useful for identifying a compound that modulates signal  
 CC transduction and for identifying a mammal having a TGR-associated  
 CC disorder. The proteins and nucleic acids are useful in diagnosis and  
 CC treatment of diseases or conditions such as renal failure, nephritis,  
 CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,  
 CC diabetes insipidus, hyperprolactinaemia and disturbances of thirst,  
 CC sleep, temperature regulation, appetite, blood pressure or any other  
 CC syndrome or disease associated with the hypothalamus. The sequences can  
 CC be used in regulation of circadian rhythms, for use as genetic markers  
 CC for the identification of mutations associated with diseases resulting  
 CC from GPCR inactivation in particular cell types and for identification of  
 CC modulators of GPCR signal transduction. This sequence represents the  
 CC human TGR342 polypeptide

XX SQ  
 XX Sequence 340 AA;

Query Match 100.0%; Score 1798; DB 5; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPFHASCWNTSAELLNKNKKEFAQTASVDTVLPSMIGICSTGLVGNILIVFTII 60

DB 1 MNPFHASCWNTSAELLNKNKKEFAQTASVDTVLPSMIGICSTGLVGNILIVFTII 60

QY 61 RSRKKTVPDIYICNLAVDLVHVGPFLLHQAQGEWVFGPGLCTIITSLDTCNQFAC 120

DB 61 RSRKKTVPDIYICNLAVDLVHVGPFLLHQAQGEWVFGPGLCTIITSLDTCNQFAC 120

QY 121 SAIMTVMVDVRYFALVQPPFLTWRTYKTRINLGLWAASFTILAPVWVYKVIKFDG 180

DB 121 SAIMTVMVDVRYFALVQPPFLTWRTYKTRINLGLWAASFTILAPVWVYKVIKFDG 180

QY 181 VESCAFDTSPDDVLWYTLTYLTITTTFFPLPLVLCYIILCYTWBYQNKDARCCNPS 240

DB 181 VESCAFDTSPDDVLWYTLTYLTITTTFFPLPLVLCYIILCYTWBYQNKDARCCNPS 240

QY 241 VPQRVMKLTQWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFVGVYLSICLSYASSS 300

DB 241 VPQRVMKLTQWLVLVVVFILSAAPYHVIQVNLQMEQPTLAFVGVYLSICLSYASSS 300

QY 301 INPFYIILSGNFQKRLPQIORRATEKEINNNNGNTLKSHP 340

DB 301 INPFYIILSGNFQKRLPQIORRATEKEINNNNGNTLKSHP 340

RESULT 9  
 AAE31492  
 ID AAE31492 standard; protein; 340 AA.

XX AC  
 XX AAE31492;

XX DT  
 XX 24-FEB-2003 (first entry)

XX DE  
 XX Human MCH-2R protein.

XX KW  
 XX Human; melanin-concentrating hormone type 2 receptor; MCH-2R;  
 KW body weight.

XX OS  
 XX Homo sapiens.

XX FH  
 XX Key Location/Qualifiers

XX FT  
 XX Misc-difference 20 /note= "Encoded by TGC"

XX FT  
 XX Misc-difference 24 /note= "Encoded by TGT"

XX FT  
 XX Misc-difference 29 /note= "Encoded by CTC"

XX FT  
 XX Misc-difference 30 /note= "Encoded by AGA"

XX FT  
 XX Misc-difference 31 /note= "Encoded by ATT"

XX FT  
 XX Misc-difference 35 /note= "Encoded by ATC"

XX FT  
 XX Misc-difference 47 /note= "Encoded by ATG"

XX FT  
 XX Misc-difference 53 /note= "Encoded by GTC"

XX FT  
 XX Misc-difference 67 /note= "Encoded by ATT"

XX FT  
 XX Misc-difference 84 /note= "Encoded by ATT"

XX FT  
 XX Misc-difference 133 /note= "Encoded by TTG"

XX FT  
 XX Misc-difference 143 /note= "Encoded by AGT"

XX FT  
 XX Misc-difference 196 /note= "Encoded by CGG"

XX FT  
 XX Misc-difference 237 /note= "Encoded by TAC"

XX FT  
 XX Misc-difference 244 /note= "Encoded by GAG"

XX FT  
 XX Misc-difference 258 /note= "Encoded by GCA"

XX FT  
 XX Misc-difference 285 /note= "Encoded by CAT"

XX FT  
 XX Misc-difference 294 /note= "Encoded by TTC"

XX FT  
 XX Misc-difference 308 /note= "Encoded by ATG"

XX FT  
 XX Misc-difference 314 /note= "Encoded by CGG"

XX FT  
 XX Misc-difference 320 /note= "Encoded by GTG"

XX FT  
 XX Misc-difference 324 /note= "Encoded by GTG"

XX FT  
 XX Misc-difference 327 /note= "Encoded by AGG"

XX PN  
 XX WO200297394-A2.



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PD 05-DEC-2002.
XX
XX
XX 28-MAY-2002; 2002WO-US016702.
XX
XX 31-MAY-2001; 2001US-0294747P.
XX
XX (MERI ) MERCK & CO INC.
XX (BANY ) BANYU PHARM CO LTD.
XX
XX Tan C, Sano H;
XX
XX WPI; 2003-047225/04.
XX DR N-PSDB; AAD48423.
XX
XX Novel melanin-concentrating hormone type 2 receptor useful in monitoring
XX body weight.
XX
XX PS Disclosure; Col 44; 26pp; English.
XX
XX The present invention relates to novel melanin-concentrating hormone type
XX 2 receptor (MCH-2R) proteins and polynucleotides encoding such proteins.
XX MCH-2R is a G-protein coupled receptor that responds to MCH and is
XX distinct from MCH-1R. Sequences of the invention are useful in measuring
XX and monitoring body weight. The present sequence is human MCH-2R protein
XX
XX SQ Sequence 340 AA;
XX
XX Query Match 100.0%; Score 1798; DB 6; Length 340;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-196;
XX Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MNPFHASCWNTSAELLNKSNNKEFAQTASVVDVILPSMIGIICSTGLVGNILIVFTII 60
XX DB 1 MNPFHASCWNTSAELLNKSNNKEFAQTASVVDVILPSMIGIICSTGLVGNILIVFTII 60
XX
XX QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPLCTIITSIDTCNQFAC 120
XX DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPLCTIITSIDTCNQFAC 120
XX
XX QY 121 SAITMVSVDYFALVQPFRLTRWRTYKTIIRINLGLWAASFILALPVWYVKVIFKDG 180
XX DB 121 SAITMVSVDYFALVQPFRLTRWRTYKTIIRINLGLWAASFILALPVWYVKVIFKDG 180
XX
XX QY 181 VESCAFDLTSPDDVLWYLYLTITTTFFPPLILVCYILILCYTWEMYOQNKDARCCNPS 240
XX DB 181 VESCAFDLTSPDDVLWYLYLTITTTFFPPLILVCYILILCYTWEMYOQNKDARCCNPS 240
XX
XX QY 241 VPQRVWMLTKWLVLVVWVFLSAAPYHVIQLVNLQMEQPTLAFYVGYVLSICLSYASSS 300
XX DB 241 VPQRVWMLTKWLVLVVWVFLSAAPYHVIQLVNLQMEQPTLAFYVGYVLSICLSYASSS 300
XX
XX QY 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHP 340
XX DB 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHP 340
XX
XX RESULT 10
XX AAE14795
XX ID AAE14795 standard; protein; 340 AA.
XX
XX AC AAE14795;
XX
XX XX 24-FEB-2003 (first entry)
XX
XX Human melanin concentrating hormone type 2 receptor (MCH2R).
XX
XX Melanin concentrating hormone type 2 receptor; MCH2R; hyperphagic;
XX hypophagic; body weight; locomotor activity; stress; anxiety;
XX sleep disorder; fatigue; circadian rhythm; energy metabolism; pain;
XX cancer; sexual dysfunction; diabetes; human.
XX
XX OS Homo sapiens.
XX
XX
XX WO200277168-A2.
XX
XX 03-OCT-2002.
XX
XX 19-MAR-2002; 2002WO-US008413.
XX
XX 22-MAR-2001; 2001US-0278061P.
XX (MERI ) MERCK & CO INC.
XX
XX Qian S, Marsh DJ;
XX
XX WPI; 2003-018901/01.
XX DR N-PSDB; AAD36796.
XX
XX MCHIR deficient mouse with an alteration in one or both alleles, useful
XX for screening of compounds as a research tool and for achieving useful
XX effects for locomotor activity, stress, anxiety, fatigue, circadian
XX rhythm or sleep.
XX
XX Disclosure; Page 30-31; 35pp; English.
XX
XX The invention relates to a melanin concentrating hormone type 1 receptor
XX (MCHIR) deficient mouse whose genome comprises an alteration in one or
XX both MCHIR alleles, where the alteration substantially reduces expression
XX of a functional MCHIR. The invention also relates to a method of
XX measuring the affect of a compound on a MCHIR deficient mouse and
XX hyperphagic or hypophagic activity, body weight, locomotor activity,
XX stress, anxiety, sleep, fatigue, circadian rhythm and energy metabolism.
XX The methods and composition of the present invention are useful for
XX screening of compounds that are further used as a research tool and for
XX treating weight loss or weight gain, reducing pain, stress, anxiety, and
XX treating cancer, sexual dysfunction, diabetes, locomotor deficits,
XX fatigue or sleep disorders. The present sequence is human melanin
XX concentrating hormone type 2 receptor (MCH2R) used in a method of the
XX invention
XX
XX SQ Sequence 340 AA;
XX
XX Query Match 100.0%; Score 1798; DB 6; Length 340;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-196;
XX Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MNPFHASCWNTSAELLNKSNNKEFAQTASVVDVILPSMIGIICSTGLVGNILIVFTII 60
XX DB 1 MNPFHASCWNTSAELLNKSNNKEFAQTASVVDVILPSMIGIICSTGLVGNILIVFTII 60
XX
XX QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPLCTIITSIDTCNQFAC 120
XX DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGPLCTIITSIDTCNQFAC 120
XX
XX QY 121 SAITMVSVDYFALVQPFRLTRWRTYKTIIRINLGLWAASFILALPVWYVKVIFKDG 180
XX DB 121 SAITMVSVDYFALVQPFRLTRWRTYKTIIRINLGLWAASFILALPVWYVKVIFKDG 180
XX
XX QY 181 VESCAFDLTSPDDVLWYLYLTITTTFFPPLILVCYILILCYTWEMYOQNKDARCCNPS 240
XX DB 181 VESCAFDLTSPDDVLWYLYLTITTTFFPPLILVCYILILCYTWEMYOQNKDARCCNPS 240
XX
XX QY 241 VPQRVWMLTKWLVLVVWVFLSAAPYHVIQLVNLQMEQPTLAFYVGYVLSICLSYASSS 300
XX DB 241 VPQRVWMLTKWLVLVVWVFLSAAPYHVIQLVNLQMEQPTLAFYVGYVLSICLSYASSS 300
XX
XX QY 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHP 340
XX DB 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHP 340
XX
XX RESULT 11
XX AAE35562
XX ID AAE35562 standard; protein; 340 AA.
XX
XX

```

AC AAE35562;  
 XX 17-JUN-2003 (first entry)  
 DT Human melanin-concentrating hormone-2 receptor (MCH-2R).  
 DE  
 XX Melanin-concentrating hormone-2 receptor; MCH-2R; appetite; MCH-1R;  
 KW melanin-concentrating hormone; MCH; receptor; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200297037-A2.  
 PN  
 XX 05-DEC-2002.  
 PD  
 XX 28-MAY-2002; 2002WO-US016513.  
 PF  
 XX 31-MAY-2001; 2001US-0294806P.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Bednarek M;  
 PI  
 XX WPI; 2003-201270/19.  
 DR  
 XX N-PSDB; RAD54241.  
 DR  
 XX  
 XX Novel truncated melanin-concentrating hormone analog peptide active at  
 PT melanin-concentrating hormone-2 receptor, or its labeled derivative or  
 PT salt, useful for increasing weight or appetite in a subject.  
 XX  
 XX Claim 16; Page 58; 30pp; English.  
 PS  
 XX The invention relates to truncated melanin-concentrating hormone (MCH)  
 XX analogue peptide active at melanin-concentrating hormone-2 receptor (MCH-  
 CC 2R), or its labelled derivative or salt, useful for increasing weight or  
 CC appetite in a subject. The peptide is useful for screening for a compound  
 CC able to bind MCH-2R. It is useful for increasing weight or appetite in a  
 CC subject having an MCH-2R. It is useful for measuring the ability of a  
 CC compound to decrease weight or appetite in a subject having MCH-2R. It is  
 CC useful to screen for MCH agonists, to explore differences between MCH-1R  
 CC and MCH-2R and to distinguish between the presence of MCH-1R and MCH-2R.  
 CC The present sequence is human MCH-2R protein  
 XX  
 XX Sequence 340 AA;  
 SQ  
 Query Match 100.0%; Score 1798; DB 6; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-196; Mismatches 0; Indels 0; Gaps 0;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPFFHASCWNTSAELLNKNKWEKFAVQTASVVDVILPMSMIGICTGLVGNLIVFTII 60  
 DB 1 MNPFFHASCWNTSAELLNKNKWEKFAVQTASVVDVILPMSMIGICTGLVGNLIVFTII 60  
 QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120  
 DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120  
 QY 121 SAIMTVMSVDVRYFALVOPFELTRWRYKTIIRINLGLWAASFILALPVWVYSKVIFKDG 180  
 DB 121 SAIMTVMSVDVRYFALVOPFELTRWRYKTIIRINLGLWAASFILALPVWVYSKVIFKDG 180  
 QY 181 VESCAPDLTSPDDVLYWTLTITTTFFPLPLILVYILCYTWEMYOQNKDARCNPS 240  
 DB 181 VESCAPDLTSPDDVLYWTLTITTTFFPLPLILVYILCYTWEMYOQNKDARCNPS 240  
 QY 241 VPQRVWMLTKWLVLVVWFILSAAPVHYIQLVNLQEOPTLAFYVGYLSICLSYASSS 300  
 DB 241 VPQRVWMLTKWLVLVVWFILSAAPVHYIQLVNLQEOPTLAFYVGYLSICLSYASSS 300  
 QY 301 INPFLYILLSGNFQKRLPQIQRSATEKEINNMGNTLKSHF 340  
 DB 301 INPFLYILLSGNFQKRLPQIQRSATEKEINNMGNTLKSHF 340

## RESULT 12

AAO27467  
 ID AAO27467 standard; protein; 340 AA.  
 XX  
 AC AAO27467;  
 XX  
 DT 16-OCT-2003 (first entry)  
 XX  
 DE Human melanin-concentrating hormone type 2 receptor (MCH-2R) protein.  
 XX  
 KW Human; melanin-concentrating hormone; hMCH; MCH type 1 receptor; MCH-1R;  
 KW MCH-1R agonist; anti-HIV; anabolic; immunomodulator; increasing weight;  
 KW increasing appetite; weight loss disorder; anorexia; AIDS; wasting;  
 KW cachexia; frail elderly disease; food intake;  
 KW hypothalamus neuronal cell body; lateral hypothalamus perikaryon;  
 KW zona inertia; orexigenic; MCH type 2 receptor; MCH-2R.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003060091-A2.  
 XX  
 PD 24-JUL-2003.  
 XX  
 PF 06-JAN-2003; 2003WO-US000241.  
 XX  
 PR 09-JAN-2002; 2002US-0347191P.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Bednarek MA;  
 XX  
 XX WPI; 2003-546040/51.  
 DR  
 XX New optionally substituted truncated human melanin-concentrating hormone  
 PT (hMCH) peptides are hMCH-1 agonists, useful for increasing  
 PT appetite/weight.  
 XX  
 PS Example 1; Page 20; 55pp; English.  
 XX  
 CC This invention relates to novel truncated human melanin-concentrating  
 CC hormone (hMCH) analogue peptides selectively active on the MCH type 1  
 CC receptor (MCH-1R). MCH has been localized to the neuronal cell bodies of  
 CC the hypothalamus which are implicated in the control of food intake,  
 CC including perikarya of the lateral hypothalamus and zona inertia. The  
 CC primary mode of action of MCH is to promote feeding (orexigenic). The  
 CC peptides of the invention, MCH-1R agonists, may have anti-HIV, anabolic  
 CC or immunomodulator activities. The peptides may be useful for increasing  
 CC weight/appetite in a subject having an MCH-1R. They may also be useful  
 CC for measuring the ability of a compound to decrease weight/appetite in a  
 CC subject having an MCH-1R which involves administering the peptides to the  
 CC subject to produce weight/appetite increase, administering the compound,  
 CC and measuring the change in weight or appetite of the subject. The  
 CC peptides may therefore be useful for treating disorders accompanied by  
 CC weight loss including anorexia, AIDS, wasting, cachexia and frail elderly  
 CC diseases. The invention offers the advantages of ease of synthesis and/or  
 CC increased solubility in physiological buffers. The present sequence is  
 CC the amino acid sequence of the human melanin-concentrating hormone (hMCH)  
 CC type 2 receptor (MCH-2R) against which the peptides of the invention are  
 CC specifically not targeted  
 XX  
 SQ Sequence 340 AA;  
 Query Match 100.0%; Score 1798; DB 6; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPFFHASCWNTSAELLNKNKWEKFAVQTASVVDVILPMSMIGICTGLVGNLIVFTII 60  
 DB 1 MNPFFHASCWNTSAELLNKNKWEKFAVQTASVVDVILPMSMIGICTGLVGNLIVFTII 60  
 QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFAC 120

61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEVFGGPLCTIITSLDTCNQFAC 120  
 121 SAIMTWSVDRYFALVQPFRLTRWTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
 121 SAIMTWSVDRYFALVQPFRLTRWTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
 181 VESCAFDLTSPDDVLTWYLYLTITTTFFPLPLILVCYIILCYTWEMVQONKDCRCNPS 240  
 181 VESCAFDLTSPDDVLTWYLYLTITTTFFPLPLILVCYIILCYTWEMVQONKDCRCNPS 240  
 241 VPQRVWMLTKWLVLVVVFILSAAPYHVIQLVNQLQMEOPTLAFYVGYLSICLSYASS 300  
 241 VPQRVWMLTKWLVLVVVFILSAAPYHVIQLVNQLQMEOPTLAFYVGYLSICLSYASS 300  
 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340  
 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340

## RESULT 13

ABW00463  
 ID ABW00463 standard; protein; 340 AA.

AC ABW00463;

DT 15-JAN-2004 (first entry)

DE Human G protein-coupled receptor (GPCR), HGPBMY9.

KW Human; G protein-coupled receptor; GPCR; HGPBMY9; therapy; brain; lung;  
 KW colon; testes; gastrointestinal; reproductive system; asthma; diabetes;  
 KW neotropic; gynaecological; Alzheimer's disease; neuroprotective; cancer;  
 KW receptor.

OS Homo sapiens.

PN US2003096300-A1.

PD 22-MAY-2003.

PF 26-SEP-2001; 2001US-00964923.

PR 27-SEP-2000; 2000US-0235709P.

PR 16-JAN-2001; 2001US-0261725P.

PR 02-AUG-2001; 2001US-0309625P.

PA (FEDE/) FEDER J N.

PA (MINT/) MINTIER G.

PA (RAMA/) RAMANATHAN C S.

PA (HAWK/) HAWKEN D R.

PA (CACA/) CACACE A.

PI Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A;

WPI; 2003-786987/74.

N-PSDB; AAD61085.

PT New human G-protein coupled receptor and its encoding polynucleotide  
 PT useful for treating and diagnosing conditions such as neurological  
 PT disorders and disorders of the testes.

PS Claim 11; Fig 2; Opp; English.

CC The invention relates to human G protein-coupled receptor (GPCR),  
 CC HGPBMY9 and its nucleic acid sequence. The invention is useful for  
 CC preventing, treating, or ameliorating a medical condition related to the  
 CC brain, lung, colon, testes, neural, gastrointestinal, pulmonary, or  
 CC reproductive system. Detecting mutations in HGPBMY9 DNA or determining  
 CC the level of expression of HGPBMY9 is useful in diagnosing disease.  
 CC HGPBMY9 nucleic acid, polypeptide and agents that control the level of  
 CC expression or activity of HGPBMY9 may be useful in treating conditions  
 CC such as cancer, Alzheimer's disease, asthma, and diabetes. The present  
 CC sequence is human HGPBMY9 protein

XX Sequence 340 AA;  
 SQ Query Match 100.0%; Score 1798; DB 7; Length 340;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-196;  
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNPFHASCWNTSABELLNKSNKEFAYQTASVVDVILPMSMIGIICSTGLVGNILIVFTII 60  
 DB 1 MNPFHASCWNTSABELLNKSNKEFAYQTASVVDVILPMSMIGIICSTGLVGNILIVFTII 60  
 QY 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEVFGGPLCTIITSLDTCNQFAC 120  
 DB 61 RSRKKTVPDIYICNLAVADLVHVGMPFLIHQWARGGEVFGGPLCTIITSLDTCNQFAC 120  
 QY 121 SAIMTWSVDRYFALVQPFRLTRWTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
 DB 121 SAIMTWSVDRYFALVQPFRLTRWTRYKTIRINLGLWAASFILALPVWVYKVIKFKDG 180  
 QY 181 VESCAFDLTSPDDVLTWYLYLTITTTFFPLPLILVCYIILCYTWEMVQONKDCRCNPS 240  
 DB 181 VESCAFDLTSPDDVLTWYLYLTITTTFFPLPLILVCYIILCYTWEMVQONKDCRCNPS 240  
 QY 241 VPQRVWMLTKWLVLVVVFILSAAPYHVIQLVNQLQMEOPTLAFYVGYLSICLSYASS 300  
 DB 241 VPQRVWMLTKWLVLVVVFILSAAPYHVIQLVNQLQMEOPTLAFYVGYLSICLSYASS 300  
 QY 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340  
 DB 301 INPFYILLSGNFQKRLPQIQRATEKEINNMGNTLKSHF 340

## RESULT 14

ABB07986  
 ID ABB07986 standard; protein; 340 AA.

XX ABB07986;

DT 12-AUG-2002 (first entry)

DE Human seven transmembrane receptor, 58875 protein.

KW Human; seven transmembrane domain receptor; 65499; 58875; cytostatic;  
 KW osteopathic; vasotropic; cardiant; antipsoriatic; antithyroid; receptor;  
 KW neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic;  
 KW antirheumatic; antiarthritic; anorectic; immunomodulator; gene therapy.

OS Homo sapiens.

PN WO200228901-A2.

PD 11-APR-2002.

PF 03-OCT-2001; 2001WO-US031250.

PR 05-OCT-2000; 2000US-0237700P.

PA (WILL-) MILLENNIUM PHARM INC.

PI Gluckmann MA;

WPI; 2002-444096/47.

N-PSDB; ABL41165, ABL41166.

PT Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane  
 PT domain receptors, useful as reagents or targets for treatment or  
 PT diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's  
 PT disease, obesity.

PS Claim 4; Fig 8; 132pp; English.

CC The invention relates to novel seven transmembrane domain receptors,  
 CC designated 65499 or 58875. The 65499 and 58875 polypeptides can be

expressed by standard recombinant methodology. The polypeptides, encoding CC polynucleotides and modulators are useful for controlling G protein CC coupled receptor-related disorders, and as a novel diagnostic target and CC therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated CC or related disorders such as cellular proliferative and differentiative CC disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism CC disorders (e.g., osteoporosis, rickets), haematopoietic disorders (such CC as chronic myelogenous leukemia, acute promyeloid leukemia), CC cardiovascular disorders (e.g., ischaemic heart disease, myocardial CC infarction, etc), endothelial cell disorder (e.g., peoriasis, Grave's CC disease), brain disorders (e.g., multiple sclerosis, Parkinson's CC disease), hormonal disorders (diabetes mellitus, hyperthyroidism), CC immune disorders (including autoimmune diseases such as rheumatoid CC arthritis, osteoarthritis), liver disorders, viral diseases such as CC hepatocellular cancer, pain disorders (e.g., pain associated with surgery CC or chest pain), metabolic disorders (obesity, cachexia). The 65499 or CC 58875 molecules are useful as surrogate markers, as pharmacodynamic CC markers and as pharmacogenomic markers. The present sequence represents CC the human 58875 protein

XX SQ Sequence 340 AA;

Query Match 99.7%; Score 1793; DB 5; Length 340;  
Best Local Similarity 99.7%; Pred. No. 2e-195;  
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPFHASCWNTSABLLNKSNNKEPAYQTASVDTVILPMSIGICSTGLVGNILIVFTII 60  
DB 1 MNPFHASCWNTSABLLNKSNNKEPAYQTASVDTVILPMSIGICSTGLVGNILIVFTII 60

QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGPLCTIITSLDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGPLCTIITSLDTCNQFAC 120

QY 121 SAIMTVMSVDRYFALVQPFRLTRWTRYKTIINLGLWAASFILALPVWYVKIFKDG 180  
DB 121 SAIMTVMSVDRYFALVQPFRLTRWTRYKTIINLGLWAASFILALPVWYVKIFKDG 180

QY 181 VESCAFDLTSPDDVLYWTLTYITITFFFPPLILVCVILCYTWEMQONKQDARCCNPS 240  
DB 181 VESCAFDLTSPDDVLYWTLTYITITFFFPPLILVCVILCYTWEMQONKQDARCCNPS 240

QY 241 VPKQRMKLTQKVLVWVVFILSAAPYHVTLQNLQWQEQTLAFYGVYILSICLSYASS 300  
DB 241 VPKQRMKLTQKVLVWVVFILSAAPYHVTLQNLQWQEQTLAFYGVYILSICLSYASS 300

QY 301 INPFLYILLSGNFQKRLPQIQRATEKEINNMGNTLKS HF 340  
DB 301 INPFLYILLSGNFQKRLPQIQRATEKEINNMGNTLKS HF 340

RESULT 15  
ID ABP81746  
AC ABP81746 standard; protein; 340 AA.  
XX  
XX  
XX 04-MAR-2003 (first entry)  
XX Human G protein-coupled receptor SLT/MCH2 protein SEQ ID NO:656.  
XX  
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.

OS Homo sapiens.  
XX WO200261087-A2.  
XX 08-AUG-2002.  
XX 19-DEC-2001; 2001WO-US050107.  
XX 19-DEC-2000; 2000US-0257144P.  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX Burner GC, Roush CL, Brown JP;  
XX WPI: 2003-046718/04.  
XX N-PSDB; ABZ42591.  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX Disclosure; Fig 1; 523pp; English.  
XX The present invention describes antigenic peptides (I) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related diseases, immunological-related diseases, cell  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention

XX SQ Sequence 340 AA;

Query Match 99.7%; Score 1792; DB 6; Length 340;  
Best Local Similarity 99.7%; Pred. No. 2.6e-195;  
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNPFHASCWNTSABLLNKSNNKEPAYQTASVDTVILPMSIGICSTGLVGNILIVFTII 60  
DB 1 MNPFHASCWNTSABLLNKSNNKEPAYQTASVDTVILPMSIGICSTGLVGNILIVFTII 60

QY 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGPLCTIITSLDTCNQFAC 120  
DB 61 RSRKKTVPDIYICNLAVADLVHIVGMPFLIHQWARGGEWFGPLCTIITSLDTCNQFAC 120

QY 121 SAIMTVMSVDRYFALVQPFRLTRWTRYKTIINLGLWAASFILALPVWYVKIFKDG 180  
DB 121 SAIMTVMSVDRYFALVQPFRLTRWTRYKTIINLGLWAASFILALPVWYVKIFKDG 180

QY 181 VESCAFDLTSPDDVLYWTLTYITITFFFPPLILVCVILCYTWEMQONKQDARCCNPS 240  
DB 181 VESCAFDLTSPDDVLYWTLTYITITFFFPPLILVCVILCYTWEMQONKQDARCCNPS 240

QY 241 VPKQRMKLTQKVLVWVVFILSAAPYHVTLQNLQWQEQTLAFYGVYILSICLSYASS 300

Db 241 VPKQXVWMLTKMVLVLLVVVFIILSAAPYHVIOVLNQLMEQPTLAFYVGVYLSICLSYASS 300  
Qy 301 INPFYILLSCNFOKELPOIORRATEKEINNMGNTLKSHF 340  
Db 301 INPFYILLSGNFQKRLPOIORRATEKEINNMGNTLKSHF 340

Search completed: May 13, 2004, 16:18:27  
Job time : 61 secs



Result No.	Score	Query Match	Length	DB ID	Description
1	1798	100.0	340	4	US-09-712-368-1
2	569.5	31.7	353	3	US-09-224-426-4
3	569.5	31.7	353	3	US-09-478-601-4
4	569.5	31.7	353	3	US-09-478-602-4
5	565.5	31.5	353	3	US-08-984-288-2
6	565.5	31.5	353	4	US-09-218-467B-2
7	565.5	31.5	400	5	PCT-US95-16472-2
8	565.5	31.5	402	3	US-08-602-809-2
9	565.5	31.5	402	4	US-09-170-496D-52
10	565.5	31.5	422	3	US-09-224-426-2
11	565.5	31.5	422	3	US-09-478-601-2
12	565.5	31.5	422	3	US-09-478-602-2
13	560.5	31.2	402	4	US-09-170-496D-192
14	456.5	25.4	418	1	US-07-816-283-10
15	456.5	25.4	418	1	US-08-417-103-10
16	449	25.0	391	1	US-07-816-283-2
17	449	25.0	391	1	US-07-816-283-4
18	449	25.0	391	1	US-08-417-103-2
19	449	25.0	391	1	US-08-417-103-4
20	449	25.0	391	1	US-08-417-103-14
21	448	24.9	391	3	US-08-420-601B-8
22	440.5	24.5	389	3	US-08-430-286A-7
23	440.5	24.5	428	1	US-07-816-283-12
24	440.5	24.5	428	1	US-08-417-103-12
25	434	24.1	369	1	US-07-816-283-6
26	434	24.1	369	1	US-08-417-103-6
27	434	24.1	369	1	US-08-417-103-16

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Db 241 VPQKRVKMLTKGVLLVWVVFILSAAPHVIVQLVNLQWQPTLAFYVGYVYLSICLSYASSS 300
Qy 301 INPFLYILLSGNFQKRLPQIQRATEKEKEINNMGNTLKSHF 340
Db 301 INPFLYILLSGNFQKRLPQIQRATEKEKEINNMGNTLKSHF 340

RESULT 2
US-09-224-426-4
; Sequence 4, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE OF INVENTION: Receptor (MCH1) And Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/224,426
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: rat
; ORGANISM: rat
US-09-224-426-4

Query Match 31.7%; Score 569.5; DB 3; Length 353;
Best Local Similarity 36.7%; Pred. No. 6.1e-45;
Matches 114; Conservative 60; Mismatches 114; Indels 23; Gaps 4;

Qy 35 VILPSMIGIICSTGLVGNILIVFTIIRSRK-----KTVPDIVICNLAVADLVHVGMPFLI 90
Db 41 IIMPSVFGTICLLGIVGNSVIFAVVKSKLHWCNSNVPDIFINLSVVDLLFLGMPFMI 100
Qy 91 HQWARGGEWVFGGPGPLCTIITSLDTCNQFACSAIMVMSVDRYFALVOPFLTRWRTRYKT 150
Db 101 HOLMGNGVWHFGETMCTLIITANDANSQFTSYILTATIDRYLATVHPISSTKFKPSMA 160
Qy 151 IRINLGLWAASFILALPVWYVKVFKDGVESCAFDLTSPD-DVLWYLYLTITTTFFFP 209
Db 161 TLVICLLWALSFSISITPVWLYARLIPPGGAVGCGIRLPNDPDLWYFTLYQFFLAFALP 220
Qy 210 LPLILVCYIILCYTWEMYQONKDCNCPSPV-----KQVWMLTKMVLVAVVVFILS 263
Db 221 FVVTAAVVKIL-----QRTSSVAPASQSRIRLTKRVRTTAICLVFFVC 268
Qy 264 AAPYHVIQVLNLQWQPTLAFYVGYVYLSICLSYASSINPFLYILLSGNFQKRLPQIQR 323
Db 269 WAPYVVLQTLQSLSRPTLTFVLYNAAISLGVANSCLNPFVYIVLCETFRKRLVLSVKP 328
Qy 324 ATEKEINNMGN 334
Db 329 AAQQLRTVSN 339

RESULT 3
US-09-478-601-4
; Sequence 4, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 574532/JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
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; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; ORGANISM: Rattus norvegicus
US-09-478-601-4

Query Match 31.7%; Score 569.5; DB 3; Length 353;
Best Local Similarity 36.7%; Pred. No. 6.1e-45;
Matches 114; Conservative 60; Mismatches 114; Indels 23; Gaps 4;

Qy 35 VILPSMIGIICSTGLVGNILIVFTIIRSRK-----KTVPDIVICNLAVADLVHVGMPFLI 90
Db 41 IIMPSVFGTICLLGIVGNSVIFAVVKSKLHWCNSNVPDIFINLSVVDLLFLGMPFMI 100
Qy 91 HQWARGGEWVFGGPGPLCTIITSLDTCNQFACSAIMVMSVDRYFALVOPFLTRWRTRYKT 150
Db 101 HOLMGNGVWHFGETMCTLIITANDANSQFTSYILTATIDRYLATVHPISSTKFKPSMA 160
Qy 151 IRINLGLWAASFILALPVWYVKVFKDGVESCAFDLTSPD-DVLWYLYLTITTTFFFP 209
Db 161 TLVICLLWALSFSISITPVWLYARLIPPGGAVGCGIRLPNDPDLWYFTLYQFFLAFALP 220
Qy 210 LPLILVCYIILCYTWEMYQONKDCNCPSPV-----KQVWMLTKMVLVAVVVFILS 263
Db 221 FVVTAAVVKIL-----QRTSSVAPASQSRIRLTKRVRTTAICLVFFVC 268
Qy 264 AAPYHVIQVLNLQWQPTLAFYVGYVYLSICLSYASSINPFLYILLSGNFQKRLPQIQR 323
Db 269 WAPYVVLQTLQSLSRPTLTFVLYNAAISLGVANSCLNPFVYIVLCETFRKRLVLSVKP 328
Qy 324 ATEKEINNMGN 334
Db 329 AAQQLRTVSN 339

RESULT 4
US-09-478-602-4
; Sequence 4, Application US/09478602
; Patent No. 6291195
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE OF INVENTION: Receptor (MCH1) And Uses Thereof
; FILE REFERENCE: 574532/JPW
; CURRENT APPLICATION NUMBER: US/09/478,602
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; ORGANISM: Rattus norvegicus
US-09-478-602-4

Query Match 31.7%; Score 569.5; DB 3; Length 353;
Best Local Similarity 36.7%; Pred. No. 6.1e-45;
Matches 114; Conservative 60; Mismatches 114; Indels 23; Gaps 4;

Qy 35 VILPSMIGIICSTGLVGNILIVFTIIRSRK-----KTVPDIVICNLAVADLVHVGMPFLI 90
Db 41 IIMPSVFGTICLLGIVGNSVIFAVVKSKLHWCNSNVPDIFINLSVVDLLFLGMPFMI 100
Qy 91 HQWARGGEWVFGGPGPLCTIITSLDTCNQFACSAIMVMSVDRYFALVOPFLTRWRTRYKT 150
Db 101 HOLMGNGVWHFGETMCTLIITANDANSQFTSYILTATIDRYLATVHPISSTKFKPSMA 160
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: GENERAL INFORMATION:
: APPLICANT: Bergsma, Derk J
: APPLICANT: Ellis, Catherine E
: TITLE OF INVENTION: Human Somatostatin Receptor
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation/Corporate
: ADDRESSEE: Intellectual Proper
: STREET: P. O. Box 1539-UW2220
: CITY: King of Prussia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19406-0939
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOCS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/16472
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Sutton, Jeffrey A
: REGISTRATION NUMBER: 34,028
: REFERENCE/DOCKET NUMBER: P50277
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610 270 5024
: TELEFAX: 610 270 5090
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 400 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-16472-2

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[illegible]

RESULT 8  
US-08-602-809-2  
; Sequence 2, Application US/08602809  
; Patent No. 6008012  
; GENERAL INFORMATION:  
; APPLICANT: BERGSMÄ, DERK

APPLICANT: ELLIS, CATHERINE  
 TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R  
 TITLE OF INVENTION: RECEPTOR  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ratner & Prestia  
 STREET: P.O. Box 980  
 CITY: Valley Forge  
 STATE: PA  
 COUNTRY: US  
 ZIP: 19482-0980  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/602,809  
 FILING DATE: 13-JUN-1997  
 CLASSIFICATION: 536  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/16472  
 FILING DATE: 15-DEC-1995  
 APPLICATION NUMBER: US 08/357,675  
 FILING DATE: 16-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Prestia, Paul F  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: P50277  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 601-407-0700  
 TELEFAX: 610-407-0701  
 TELEX: 846169  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 402 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-602-809-2

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Query Match      31.5%; Score 565.5; DB 3; Length 402;
Best Local Similarity 36.3%; Pred. No. 1.6e-44;
Matches 113; Conservative 61; Mismatches 114; Indels 23; Gaps 4;

Qy   35 VILPSWIGIICTGLGVGNLIVFLIIBSRK-----KVDPDIYICNLAVADLVHIVGMPPLI 90
Db   90 IIMPVSFGTICLLGIIGNSTVIFAWKKSLHKWCNNVPDIFINISVDLLEFLLGMPFI 144
Qy   91 HQWARGGSWFVGGLPTIITSLDTCNCFACSAIMTVMSVDRYFALVQPPRLTFEWRTRYKT 150
Db   150 HQLMNGVWHFHGETWKTCILITAMDANSOFTSYILTAMADRVLATVHPPISSIKFKRPSVA 209
Qy   151 IRINLGUNAASFIALLPWNYSVKVIFPKGVESCAFDLTSPD-DVLWYTYLYITITFFPPP 209
Db   210 TLVICLLWALSFSISTPWLYARLIIPPGGAVGGIRLENPDTDLYWFYTLGYQFFLAFLAP 269
Qy   210 LPLLVCYLILCYTWEMYQNCKDKACCNSVP-----KQRWMLKTMXVLVLVVVFLLS 263
Db   270 FVIIITAAVRIL-----QRMTSSVAPASORSIRLTRTKRVTRTAICAICLVFPVC 317
Qy   264 AAPYHVIOQLVNLMEOPTLAFVGVGYLSICLSYASSINPFYILLSGNFOKRLPQIQRR 323
Db   318 WAPYVVLQLTOLTSRFTLIFVLYNRAAISLGVANSLNPFFVIYCETFRKLVLVSKP 377
Qy   324 ATEKEINNMGN 334
Db   378 AAQGOLRAVSN 388

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RESULT 9  
US-09-170-496D-52

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; Sequence 52, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-170-496D-52

Query Match      31.5%; Score 565.5; DB 4; Length 402;
Best Local Similarity 36.3%; Pred. No. 1.7e-44;
Matches 113; Conservative 61; Mismatches 114; Indels 23; Gaps 4;

QY      35 VILPSMIGIICSTGLVGNILIVFTIIRSK-----KTPVDIYICNLAVADLVHIVGMPFLI 90
Db      110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLLGMPFMI 169

QY      91 HQWARGGEWFGGPGPLCTIITSLDTCNQFACSAIMTVMSVDYFALVQPFRLTRWRTRYKT 150
Db      170 HQLMGNGVWHFGETMCTLTITAMDANSQFTSYILTAMADRYLATVHPISSTKFKRPSVA 229

QY      151 IRINLGLWAASFILALPVWVYSKVIKFGDGVESCAFDTLSPD-DVLWYTYLYTITITFFPP 209
Db      230 TLVICLLWALSFSITPWLYARLIPPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALP 289

QY      210 LPLILVCYILILCYTWEMYQONKDACCNPSVP-----KQVVKLTVMVLVUVVFI 263
Db      290 FVWITAAYVRIL-----QRMTSVAPASQSRIRLTKRVTRTAICLVFFVC 337

QY      264 AAPYHVIQLVNLQMEOPTLAFYVGYLSICLSYASSINPFYLLSGNFQKRLPQIQRR 323
Db      338 WAPYVVLQTLQLSISRPTLTFFVLYNAAISLGVANSCLNPFVYIVLCETFRKRLVLSVKP 397

QY      324 ATEKEINNMGN 334
Db      378 AAQGLRAVSN 388

RESULT 10
US-09-224-426-2
; Sequence 2, Application US/09224426
; Patent No. 6221613
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 57453/JPW/JHE
; CURRENT APPLICATION NUMBER: US/09/224,426
; CURRENT FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-224-426-2

Query Match      31.5%; Score 565.5; DB 3; Length 422;
Best Local Similarity 36.3%; Pred. No. 1.7e-44;
Matches 113; Conservative 61; Mismatches 114; Indels 23; Gaps 4;

QY      35 VILPSMIGIICSTGLVGNILIVFTIIRSK-----KTPVDIYICNLAVADLVHIVGMPFLI 90
Db      110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLLGMPFMI 169

QY      91 HQWARGGEWFGGPGPLCTIITSLDTCNQFACSAIMTVMSVDYFALVQPFRLTRWRTRYKT 150
Db      170 HQLMGNGVWHFGETMCTLTITAMDANSQFTSYILTAMADRYLATVHPISSTKFKRPSVA 229

QY      151 IRINLGLWAASFILALPVWVYSKVIKFGDGVESCAFDTLSPD-DVLWYTYLYTITITFFPP 209
Db      230 TLVICLLWALSFSITPWLYARLIPPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALP 289

QY      210 LPLILVCYILILCYTWEMYQONKDACCNPSVP-----KQVVKLTVMVLVUVVFI 263
Db      290 FVWITAAYVRIL-----QRMTSVAPASQSRIRLTKRVTRTAICLVFFVC 337

QY      264 AAPYHVIQLVNLQMEOPTLAFYVGYLSICLSYASSINPFYLLSGNFQKRLPQIQRR 323
Db      338 WAPYVVLQTLQLSISRPTLTFFVLYNAAISLGVANSCLNPFVYIVLCETFRKRLVLSVKP 397
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; Sequence 52, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-170-496D-52

Query Match      31.5%; Score 565.5; DB 4; Length 402;
Best Local Similarity 36.3%; Pred. No. 1.7e-44;
Matches 113; Conservative 61; Mismatches 114; Indels 23; Gaps 4;

QY      35 VILPSMIGIICSTGLVGNILIVFTIIRSK-----KTPVDIYICNLAVADLVHIVGMPFLI 90
Db      110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLLGMPFMI 169

QY      91 HQWARGGEWFGGPGPLCTIITSLDTCNQFACSAIMTVMSVDYFALVQPFRLTRWRTRYKT 150
Db      170 HQLMGNGVWHFGETMCTLTITAMDANSQFTSYILTAMADRYLATVHPISSTKFKRPSVA 229

QY      151 IRINLGLWAASFILALPVWVYSKVIKFGDGVESCAFDTLSPD-DVLWYTYLYTITITFFPP 209
Db      230 TLVICLLWALSFSITPWLYARLIPPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALP 289

QY      210 LPLILVCYILILCYTWEMYQONKDACCNPSVP-----KQVVKLTVMVLVUVVFI 263
Db      290 FVWITAAYVRIL-----QRMTSVAPASQSRIRLTKRVTRTAICLVFFVC 337

QY      264 AAPYHVIQLVNLQMEOPTLAFYVGYLSICLSYASSINPFYLLSGNFQKRLPQIQRR 323
Db      338 WAPYVVLQTLQLSISRPTLTFFVLYNAAISLGVANSCLNPFVYIVLCETFRKRLVLSVKP 397

QY      324 ATEKEINNMGN 334
Db      378 AAQGLRAVSN 388

RESULT 11
US-09-478-601-2
; Sequence 2, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salton, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Nagorny, Raisa
; APPLICANT: Wilson, Amy E.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; FILE REFERENCE: 574532/JPW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-478-601-2

Query Match      31.5%; Score 565.5; DB 3; Length 422;
Best Local Similarity 36.3%; Pred. No. 1.7e-44;
Matches 113; Conservative 61; Mismatches 114; Indels 23; Gaps 4;

QY      35 VILPSMIGIICSTGLVGNILIVFTIIRSK-----KTPVDIYICNLAVADLVHIVGMPFLI 90
Db      110 IIMPSVFGTICLLGIIGNSTVIFAVVKKSKLHWCNNVPDIFINLSVVDLLFLLGMPFMI 169

QY      91 HQWARGGEWFGGPGPLCTIITSLDTCNQFACSAIMTVMSVDYFALVQPFRLTRWRTRYKT 150
Db      170 HQLMGNGVWHFGETMCTLTITAMDANSQFTSYILTAMADRYLATVHPISSTKFKRPSVA 229

QY      151 IRINLGLWAASFILALPVWVYSKVIKFGDGVESCAFDTLSPD-DVLWYTYLYTITITFFPP 209
Db      230 TLVICLLWALSFSITPWLYARLIPPPGAVGCGIRLPNPDLDLYWFTLYQFFLAFALP 289

QY      210 LPLILVCYILILCYTWEMYQONKDACCNPSVP-----KQVVKLTVMVLVUVVFI 263
Db      290 FVWITAAYVRIL-----QRMTSVAPASQSRIRLTKRVTRTAICLVFFVC 337

QY      264 AAPYHVIQLVNLQMEOPTLAFYVGYLSICLSYASSINPFYLLSGNFQKRLPQIQRR 323
Db      338 WAPYVVLQTLQLSISRPTLTFFVLYNAAISLGVANSCLNPFVYIVLCETFRKRLVLSVKP 397
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US-08-417-103-10
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Best Local Similarity 32.4%; Pred. No. 2.1e-34;
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DB 1 MDMLHPSSVSTSEPENASSAMPDPATLGNVSAGSPAGLAVSGVLIPLVYLVCVWGLL 60
QY 51 GNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMFPLIHOWARGGEWVFGGPLCTII 109
DB 61 GNSLVIYVVLRLHTASPSVTNVYILNALADELFMLGLPFLAAQNAL-SYWPFGSLMCLV 119
QY 110 TSLDTCNQFACSAIMTVMSVDRYFALVOPFLTRWTRYKTIIRINLGLWAASFILALPVM 169
DB 120 MAVDGINQFTSIFCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSAAVVVASAVVLPVV 179
QY 170 VYSKVIKFGDVESCAFDLTSPDDVLW---YTLVLTITTTFFPLPLILVCYLICYTWE 226
DB 180 VFSGVPR---GMSTCHQWPEP-AAAWRAGFIITYAALGFFGLLIVCLCCLLVIV----- 230
QY 227 MYQCKNDARCCNPSVPKQR--VMKLTQVLLVVLVVFILSAAPYHVIQNLQW---EQPT 281
DB 231 VKVRSAGRWAPSCORRRRSERVRTRMVAVVAVLFLVCMWPFYVLNINNVVCPLEP- 289
QY 282 LAFYVGYVLSICLSYASSINPPLYILLSGNFQKRLPQIQRATEK 327
DB 290 -AFFGLYFLVVALPYANSCANPILYGLSYRFKQGRVRLRPSSR 334
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Search completed: May 13, 2004, 16:21:03  
Job time : 24 secs

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MOLECULE TYPE: protein
US-07-816-283-10
Query Match 25.4%; Score 456.5; DB 1; Length 418;
Best Local Similarity 32.4%; Pred. No. 2.1e-34;
Matches 112; Conservative 75; Mismatches 128; Indels 31; Gaps 11;
QY 1 MNPFFASCWNTSAELINKS--WNKEFAYQTAS-----VVDTVILPSMIGIICSTGLV 50
DB 1 MDMLHPSSVSTSEPENASSAMPDPATLGNVSAGSPAGLAVSGVLIPLVYLVCVWGLL 60
QY 51 GNILIVFTIIR-SRKKTVPDIYICNLAVADLVHIVGMFPLIHOWARGGEWVFGGPLCTII 109
DB 61 GNSLVIYVVLRLHTASPSVTNVYILNALADELFMLGLPFLAAQNAL-SYWPFGSLMCLV 119
QY 110 TSLDTCNQFACSAIMTVMSVDRYFALVOPFLTRWTRYKTIIRINLGLWAASFILALPVM 169
DB 120 MAVDGINQFTSIFCLTVMSVDRYLAVVHPTRSARWRTAPVARTVSAAVVVASAVVLPVV 179
QY 170 VYSKVIKFGDVESCAFDLTSPDDVLW---YTLVLTITTTFFPLPLILVCYLICYTWE 226
DB 180 VFSGVPR---GMSTCHQWPEP-AAAWRAGFIITYAALGFFGLLIVCLCCLLVIV----- 230
QY 227 MYQCKNDARCCNPSVPKQR--VMKLTQVLLVVLVVFILSAAPYHVIQNLQW---EQPT 281
DB 231 VKVRSAGRWAPSCORRRRSERVRTRMVAVVAVLFLVCMWPFYVLNINNVVCPLEP- 289
QY 282 LAFYVGYVLSICLSYASSINPPLYILLSGNFQKRLPQIQRATEK 327
DB 290 -AFFGLYFLVVALPYANSCANPILYGLSYRFKQGRVRLRPSSR 334
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RESULT 15  
US-08-417-103-10  
; Sequence 10, Application US/08417103  
; Patent No. 5723299  
; GENERAL INFORMATION:  
; APPLICANT: Bell, Graeme I.  
; APPLICANT: Yamada, Yuichiro  
; APPLICANT: Sano, Susumu  
; TITLE OF INVENTION: SOMATOSTATIN RECEPTORS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,103  
; FILING DATE: 05-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/816,283  
; FILING DATE: 01-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:144  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 418 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 20:37:38 ; Search time 504 Seconds  
(without alignments)  
9211.159 Million cell updates/sec

Title: US-09-913-770B-2  
Perfect score: 1023  
Sequence: 1 atgaatccatttcgacgc.....ctctgaaatcacacttttag 1023

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
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9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
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14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
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18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1023	100.0	1023	10	US-09-964-923A-1
3	1023	100.0	1023	15	US-10-321-807-39
4	1023	100.0	1023	17	US-10-332-082-9
5	1023	100.0	1035	17	US-10-332-082-4
6	1023	100.0	1965	10	US-09-791-932-57
7	1021.4	99.8	1023	10	US-09-971-269-6
8	1021.4	99.8	1278	10	US-09-971-269-3
9	1021.4	99.8	1330	15	US-10-225-567A-665
10	987.8	96.6	1023	15	US-10-309-515-37
11	987.8	96.6	1023	15	US-10-291-990-5
12	987.8	96.6	1023	15	US-10-126-764-37
13	984.6	96.2	1023	15	US-10-309-515-33
14	984.6	96.2	1023	15	US-10-291-990-1

15	984.6	96.2	1023	15	US-10-126-764-33	Sequence 33, Appl
16	983	96.1	1023	15	US-10-309-515-35	Sequence 35, Appl
17	983	96.1	1023	15	US-10-291-990-3	Sequence 3, Appl
18	983	96.1	1023	15	US-10-126-764-35	Sequence 35, Appl
19	981.4	95.9	1558	17	US-10-333-946-30	Sequence 30, Appl
20	934.6	81.6	993	15	US-10-309-515-38	Sequence 38, Appl
21	934.6	81.6	993	15	US-10-291-990-6	Sequence 6, Appl
22	934.6	81.6	993	15	US-10-126-764-38	Sequence 38, Appl
23	716	70.0	757	17	US-10-332-082-5	Sequence 5, Appl
24	484.2	47.3	546	13	US-10-052-283-430	Sequence 430, App
25	230.2	22.5	1080	15	US-10-309-515-49	Sequence 49, Appl
26	230.2	22.5	1080	15	US-10-126-764-49	Sequence 49, Appl
27	216.6	21.2	1044	15	US-10-309-515-59	Sequence 59, Appl
28	215.4	21.1	735	10	US-09-791-279-11	Sequence 11, Appl
29	195.6	19.1	1038	15	US-10-309-515-51	Sequence 51, Appl
30	195.6	19.1	1038	15	US-10-126-764-51	Sequence 51, Appl
31	191.6	18.7	1059	15	US-10-309-515-47	Sequence 47, Appl
32	191.6	18.7	1059	15	US-10-126-764-47	Sequence 47, Appl
33	182.4	17.8	591	10	US-09-791-932-11	Sequence 11, Appl
34	144.8	14.2	1062	13	US-10-333-379-6	Sequence 6, Appl
35	144.8	14.2	1074	15	US-10-276-288-4	Sequence 4, Appl
36	144.8	14.2	1074	17	US-10-258-492-4	Sequence 4, Appl
37	144.8	14.2	1074	17	US-10-332-082-18	Sequence 18, Appl
38	144.8	14.2	1214	9	US-09-885-478-3	Sequence 3, Appl
39	144.8	14.2	1214	10	US-09-899-732-3	Sequence 3, Appl
40	144.8	14.2	1214	13	US-10-341-751-3	Sequence 3, Appl
41	144.8	14.2	1214	15	US-10-029-314-3	Sequence 3, Appl
42	135.6	13.3	1349	11	US-09-826-509-358	Sequence 358, App
43	132	12.9	1062	11	US-09-826-509-386	Sequence 386, App
44	132	12.9	1062	15	US-10-309-515-16	Sequence 16, Appl
45	132	12.9	1062	15	US-10-126-764-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-990-940-1  
; Sequence 1, Application US/0990940  
; Publication No. US20030027252A1  
; GENERAL INFORMATION:  
; APPLICANT: Tian, Hui  
; APPLICANT: Zhao, Jiagang  
; APPLICANT: Chen, Jin-Long  
; APPLICANT: Cutler, Gene  
; APPLICANT: An, Songzhu  
; APPLICANT: Dai, Kang  
; APPLICANT: Gupta, Jamila S.  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: No. US20030027252A1el Receptors  
; FILE REFERENCE: 018781-007410US  
; CURRENT APPLICATION NUMBER: US/09/990,940  
; CURRENT FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/252,841  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 60/257,636  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 60/261,377  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/279,554  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/280,696  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1023)  
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR342,

OTHER INFORMATION: melanin-concentrating hormone receptor 2 (MCHR2)  
US-09-930-940-1

Query Match 100.0%; Score 1023; DB 10; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATCCATTTTCATGTCATCTTGTGGACACACCTCTGCCGAACTTTTAAACAAATCCTGG 60  
DB 1 ATGAATCCATTTTCATGTCATCTTGTGGACACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

QY 61 AATAAAGAGTTTGGTATCAAACTGCCAGTGGTAGATACAGTATCTCCCTCCCTG 120  
DB 61 AATAAAGAGTTTGGTATCAAACTGCCAGTGGTAGATACAGTATCTCCCTCCCTG 120

QY 121 ATTGGGATTTATCTGTTCAACAGGGCTGTTGGCAACATCTCTATTCTATTCTACTATAATA 180  
DB 121 ATTGGGATTTATCTGTTCAACAGGGCTGTTGGCAACATCTCTATTCTATTCTACTATAATA 180

QY 181 AGATCCAGGAAAAAAGCCTCTGACATCTATATCTGCAACCTGCTGCTGCTGATTTG 240  
DB 181 AGATCCAGGAAAAAAGCCTCTGACATCTATATCTGCAACCTGCTGCTGCTGATTTG 240

QY 241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300  
DB 241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300

QY 301 TTTGGGGGGCTCTCTGCAACCATCATCATCCTGGATATCTTGTAAACAAATTTGCTGT 360  
DB 301 TTTGGGGGGCTCTCTGCAACCATCATCATCCTGGATATCTTGTAAACAAATTTGCTGT 360

QY 361 AGTGCCATCATGACTCTGATGAGTGGACAGTACTTTGGCCCTCGTCCCAACATTTGCA 420  
DB 361 AGTGCCATCATGACTCTGATGAGTGGACAGTACTTTGGCCCTCGTCCCAACATTTGCA 420

QY 421 CTGACAGCTTTGGAGAACAAAGGTACAGACCATCCGGATCAATTTGGGCTTTTGGGAGCT 480  
DB 421 CTGACAGCTTTGGAGAACAAAGGTACAGACCATCCGGATCAATTTGGGCTTTTGGGAGCT 480

QY 481 TCCCTTTATCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 481 TCCCTTTATCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 541 GTTGAGAGTTGCTTTGATTTGATCTCCCTGACGATGATCTCTGTTATACATTTAT 600  
DB 541 GTTGAGAGTTGCTTTGATTTGATCTCCCTGACGATGATCTCTGTTATACATTTAT 600

QY 601 TTGACGATAACAACTTTTCTTACCTCTACCTTGAATTTGGTGTGCTATATTTAAT 660  
DB 601 TTGACGATAACAACTTTTCTTACCTCTACCTTGAATTTGGTGTGCTATATTTAAT 660

QY 661 TTATGCTATCTGAGAGATGATCAACAGATATAGGATGCCAGATGCTGCAATCCAGT 720  
DB 661 TTATGCTATCTGAGAGATGATCAACAGATATAGGATGCCAGATGCTGCAATCCAGT 720

QY 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGGTGTGCTGCTGCTGCTGCTGCT 780  
DB 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGGTGTGCTGCTGCTGCTGCTGCT 780

QY 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

QY 841 ACAGTGGCTTCTATGCTGGTATTACCTCTCCATCTGCTCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 841 ACAGTGGCTTCTATGCTGGTATTACCTCTCCATCTGCTCTGCTGCTGCTGCTGCTGCTGCT 900

QY 901 ATTAACCTTTTCTCTAATCTCTGCTGAGTGAATTTCCAGAAACGCTGCTGCTCAATC 960  
DB 901 ATTAACCTTTTCTCTAATCTCTGCTGAGTGAATTTCCAGAAACGCTGCTGCTCAATC 960

QY 961 CAAAGAGAGCGACTGAGAGGAATCAACATATGGGAAACACTCTGAAATCAACATTT 1020  
DB 961 CAAAGAGAGCGACTGAGAGGAATCAACATATGGGAAACACTCTGAAATCAACATTT 1020

RESULT 2  
US-09-964-923A-1  
; Sequence 1, Application US/09964923A  
; Publication No. US20030096300A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.  
; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAWKEN, D. R.  
; APPLICANT: CACACE, A.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP9MY9,  
; FILE REFERENCE: D0045NP  
; CURRENT APPLICATION NUMBER: US/09/964,923A  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/309,625  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/261,775  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/235,709  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-923A-1

Query Match 100.0%; Score 1023; DB 10; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATCCATTTTCATGTCATCTTGTGGACACACCTCTGCCGAACTTTTAAACAAATCCTGG 60  
DB 1 ATGAATCCATTTTCATGTCATCTTGTGGACACACCTCTGCCGAACTTTTAAACAAATCCTGG 60

QY 61 AATAAAGAGTTTGGTATCAAACTGCCAGTGGTAGATACAGTATCTCCCTCCCTG 120  
DB 61 AATAAAGAGTTTGGTATCAAACTGCCAGTGGTAGATACAGTATCTCCCTCCCTG 120

QY 121 ATTGGGATTTATCTGTTCAACAGGGCTGTTGGCAACATCTCTATTCTATTCTACTATAATA 180  
DB 121 ATTGGGATTTATCTGTTCAACAGGGCTGTTGGCAACATCTCTATTCTATTCTACTATAATA 180

QY 181 AGATCCAGGAAAAAAGCCTCTGACATCTATATCTGCAACCTGCTGCTGCTGATTTG 240  
DB 181 AGATCCAGGAAAAAAGCCTCTGACATCTATATCTGCAACCTGCTGCTGCTGATTTG 240

QY 241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300  
DB 241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300

QY 301 TTTGGGGGGCTCTCTGCAACCATCATCATCCTGGATATCTTGTAAACAAATTTGCTGT 360  
DB 301 TTTGGGGGGCTCTCTGCAACCATCATCATCCTGGATATCTTGTAAACAAATTTGCTGT 360

QY 361 AGTGCCATCATGACTCTGATGAGTGGACAGTACTTTGGCCCTCGTCCCAACATTTGCA 420  
DB 361 AGTGCCATCATGACTCTGATGAGTGGACAGTACTTTGGCCCTCGTCCCAACATTTGCA 420

QY 421 CTGACAGCTTTGGAGAACAAAGGTACAGACCATCCGGATCAATTTGGGCTTTTGGGAGCT 480  
DB 421 CTGACAGCTTTGGAGAACAAAGGTACAGACCATCCGGATCAATTTGGGCTTTTGGGAGCT 480

QY 481 TCCCTTTATCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
DB 481 TCCCTTTATCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 541 GTTGAGAGTTGCTTTGATTTGATCTCCCTGACGATGATCTCTGTTATACATTTAT 600  
DB 541 GTTGAGAGTTGCTTTGATTTGATCTCCCTGACGATGATCTCTGTTATACATTTAT 600

QY 601 TTGACGATAACAACTTTTCTTACCTCTACCTTGAATTTGGTGTGCTATATTTAAT 660  
DB 601 TTGACGATAACAACTTTTCTTACCTCTACCTTGAATTTGGTGTGCTATATTTAAT 660

QY 661 TTATGCTATCTGAGAGATGATCAACAGATATAGGATGCCAGATGCTGCAATCCAGT 720  
DB 661 TTATGCTATCTGAGAGATGATCAACAGATATAGGATGCCAGATGCTGCAATCCAGT 720

QY 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGGTGTGCTGCTGCTGCTGCTGCT 780  
DB 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGGTGTGCTGCTGCTGCTGCTGCT 780

QY 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

QY 841 ACAGTGGCTTCTATGCTGGTATTACCTCTCCATCTGCTCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 841 ACAGTGGCTTCTATGCTGGTATTACCTCTCCATCTGCTCTGCTGCTGCTGCTGCTGCTGCT 900

QY 901 ATTAACCTTTTCTCTAATCTCTGCTGAGTGAATTTCCAGAAACGCTGCTGCTCAATC 960  
DB 901 ATTAACCTTTTCTCTAATCTCTGCTGAGTGAATTTCCAGAAACGCTGCTGCTCAATC 960

QY 961 CAAAGAGAGCGACTGAGAGGAATCAACATATGGGAAACACTCTGAAATCAACATTT 1020  
DB 961 CAAAGAGAGCGACTGAGAGGAATCAACATATGGGAAACACTCTGAAATCAACATTT 1020







Db 7 ATGAATCCATTTCATGCATCTTGTGGAAACACCTCTGCCGAACCTTTTAAACAAATCCTGG 66  
QY 61 AATAAAGAGTTGCTTTATCAAACTGCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 120  
Db 67 AATAAAGAGTTGCTTTATCAAACTGCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 126  
QY 121 ATTGGGATTATCTGTTCAACAGGGCTGGTGGCAACATCTCTATGTATTAATCACTATAATA 180  
Db 127 ATTGGGATTATCTGTTCAACAGGGCTGGTGGCAACATCTCTATGTATTAATCACTATAATA 186  
QY 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTG 240  
Db 187 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTG 246  
QY 241 GTCCACATAGTTGGAAATGCTTTTCTTATTCACCAATGGCCCGAGAGGGGAGTGGGTG 300  
Db 247 GTCCACATAGTTGGAAATGCTTTTCTTATTCACCAATGGCCCGAGAGGGGAGTGGGTG 306  
QY 301 TTGGGGGGCTCTCTGCAACCATCATCACATCCCTGGATCTGTAAACCAATTCGCTGT 360  
Db 307 TTGGGGGGCTCTCTGCAACCATCATCACATCCCTGGATCTGTAAACCAATTCGCTGT 366  
QY 361 AGTGCCATCATGCTTAATAGTGTGGACAGTACTTTGCCCTCGTCCAACTTTTGA 420  
Db 367 AGTGCCATCATGCTTAATAGTGTGGACAGTACTTTGCCCTCGTCCAACTTTTGA 426  
QY 421 CTCACAGCTTGGAGACAGGTACAGACCATCCGATCAATTTGGGCTTTTGGCAGCT 480  
Db 427 CTCACAGCTTGGAGACAGGTACAGACCATCCGATCAATTTGGGCTTTTGGCAGCT 486  
QY 481 TCTTTATCTCTGGCATTGCTGTGGGTCTACTCGAAGGTCACTCAAAATTTAAAGACGCT 540  
Db 487 TCTTTATCTCTGGCATTGCTGTGGGTCTACTCGAAGGTCACTCAAAATTTAAAGACGCT 546  
QY 541 GTTGAGAGTTGCTTTTGAATTTGATCATCCCTGAGATGTACTCTGGTATACATTTAT 600  
Db 547 GTTGAGAGTTGCTTTTGAATTTGATCATCCCTGAGATGTACTCTGGTATACATTTAT 606  
QY 601 TTGACATTAACAACTTTTCTTCTCCCTCTACCTTGATTTTGGTGTCTATATTTAAT 660  
Db 607 TTGACATTAACAACTTTTCTTCTCCCTCTACCTTGATTTTGGTGTCTATATTTAAT 666  
QY 661 TTATGCTATCTTGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT 720  
Db 667 TTATGCTATCTTGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT 726  
QY 721 GTACCAAAACAGAGAGTGTAGTTGACAAAGATGCTGCTGCTGTGTGTACTCTTT 780  
Db 727 GTACCAAAACAGAGAGTGTAGTTGACAAAGATGCTGCTGCTGTGTGTACTCTTT 786  
QY 781 ATCCTGAGTGTGCTCCCTTTATCATGTATACAACTGGTGAACTTACAGATGGAACAGGCC 840  
Db 787 ATCCTGAGTGTGCTCCCTTTATCATGTATACAACTGGTGAACTTACAGATGGAACAGGCC 846  
QY 841 ACCTGGCTTCTATGTGGTTATTAACCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 847 ACCTGGCTTCTATGTGGTTATTAACCTCTGATCTGCTGCTGCTGCTGCTGCTGCTGCT 906  
QY 901 ATTAACCTTTTCTCTACATCTCTGCTGAGTGGAAATTTCCAGAAACGCTGCTGCTCAATC 960  
Db 907 ATTAACCTTTTCTCTACATCTCTGCTGAGTGGAAATTTCCAGAAACGCTGCTGCTCAATC 966  
QY 961 CAAAGAGAGCGACTGAGAGGAAATCAACATATGGGAAAACACTCTGAAATCACTTT 1020  
Db 967 CAAAGAGAGCGACTGAGAGGAAATCAACATATGGGAAAACACTCTGAAATCACTTT 1026  
QY 1021 TAG 1023  
Db 1027 TAG 1029

RESULT 6

US-09-791-932-57

; Sequence 57, Application US/09791932  
; Publication No. US20030003451A1

## GENERAL INFORMATION:

; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Hiebsch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kaytes, Paul S.  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.

; TITLE OF INVENTION: No. US20030003451A1el G Protein-Coupled Receptors Cross-Referer

; FILE REFERENCE: 00325.US1

; CURRENT APPLICATION NUMBER: US/09/791,932

; PRIOR FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/184,305

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,304

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,303

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,397

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/184,247

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 60/188,880

; PRIOR FILING DATE: 2000-03-13

; PRIOR APPLICATION NUMBER: 60/217,369

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/217,370

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: 60/218,492

; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: 60/186,810

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/188,064

; PRIOR FILING DATE: 2000-03-09

; PRIOR APPLICATION NUMBER: 60/186,457

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: 60/213,861

; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: 60/194,344

; PRIOR FILING DATE: 2000-04-03

; PRIOR APPLICATION NUMBER: 60/218,337

; PRIOR FILING DATE: 2000-07-14

; NUMBER OF SEQ ID NOS: 184

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 57

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-791-932-57

Query Match 100.0%; Score 1023; DB 10; Length 1965;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATCCATTTCATGCATCTTGTGGAAACACCTCTGCCGAACCTTTTAAACAAATCCTGG 60

Db 58 ATGAATCCATTTCATGCATCTTGTGGAAACACCTCTGCCGAACCTTTTAAACAAATCCTGG 117

QY 61 AATAAAGAGTTTGTCTTATCAAACTGCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 120

Db 118 AATAAAGAGTTTGTCTTATCAAACTGCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 177

QY 121 ATTGGGATTATCTGTTCAACAGGGCTGTTGGCAACATCTCTCATTTGTTATTCATATAATA 180

Db 178 ATTGGGATTATCTGTTCAACAGGGCTGTTGGCAACATCTCTCATTTGTTATTCATATAATA 237

QY 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGGTGGTGGTATTG 240

Db 238 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGGTGGTGGTATTG 297

241 GTCCACATAGTTGGAATGCTTTTCTTTATTCACCAATGGGCCCGAGGGGAGAGTGGGTG 300  
298 GTCCACATAGTTGGAATGCTTTTCTTTATTCACCAATGGGCCCGAGGGGAGAGTGGGTG 357  
301 TTTGGGGGGCTCTCTGACCATCATACATCCCTGGATCTGTAAACCAATTTGCTCTG 360  
358 TTTGGGGGGCTCTCTGACCATCATACATCCCTGGATCTGTAAACCAATTTGCTCTG 417  
361 AGTGCCATCATGACTGTAATGAGTGTGGACAGTACTTTGCCCTCTGCAACCAATTTGCA 420  
418 AGTGCCATCATGACTGTAATGAGTGTGGACAGTACTTTGCCCTCTGCAACCAATTTGCA 477  
421 CTGACAGCTTTGGAGAACAGGTACAGACCATCCGATCAATTTGGGCGCTTTGGGCGAGCT 480  
478 CTGACAGCTTTGGAGAACAGGTACAGACCATCCGATCAATTTGGGCGCTTTGGGCGAGCT 537  
481 TCCCTTATCTGCGCATTTGCTGCTGGTCTACTCGAAGGTCAATTTTAAAGACGGT 540  
538 TCCCTTATCTGCGCATTTGCTGCTGGTCTACTCGAAGGTCAATTTTAAAGACGGT 597  
541 GTTGAGAGTTGCTTTGATTTGATTCATCCCTGACGATGTACTCTGGTATACACTTTAT 600  
598 GTTGAGAGTTGCTTTGATTTGATTTGATTCATCCCTGACGATGTACTCTGGTATACACTTTAT 657  
601 TTAGCAGTAAACACTTTTTTTTTTCCCTCTACCCCTTCAATTTGGTGTGCTATATTTAAAT 660  
658 TTAGCAGTAAACACTTTTTTTTTTCCCTCTACCCCTTCAATTTGGTGTGCTATATTTAAAT 717  
661 TTAGCTATATCTTTGGAGATGTATCAACAGAAATAAGATGCTGCAATCCAGT 720  
718 TTAGCTATATCTTTGGAGATGTATCAACAGAAATAAGATGCTGCAATCCAGT 777  
721 GTACCAAAACAGAGAGTGAAGTTCAGAAAGATGGTCTGGTGTAGTCTTT 780  
778 GTACCAAAACAGAGAGTGAAGTTCAGAAAGATGGTCTGGTGTAGTCTTT 837  
781 ATCTGAGTCTGCCCCCTTATCATGTGATACAACTGGTGAACCTTACAGATGGAACAGCC 840  
838 ATCTGAGTCTGCCCCCTTATCATGTGATACAACTGGTGAACCTTACAGATGGAACAGCC 897  
841 ACATGCGCTTCTATGAGGTATATACCTCTCATCTGCTGAGCTATGCCAGCAGC 900  
898 ACATGCGCTTCTATGAGGTATATACCTCTCATCTGCTGAGCTATGCCAGCAGC 957  
901 ATTAACCTTTTCTACATCTGCTGAGTGGAAATTTCCAGAAAGCTCTGCTCAAAATC 960  
958 ATTAACCTTTTCTACATCTGCTGAGTGGAAATTTCCAGAAAGCTCTGCTCAAAATC 1017  
961 CAAGAAGAGCGACTGAGAGGAAATCAACAATATGGAACACTCTGAAATCAGACTTT 1020  
1018 CAAGAAGAGCGACTGAGAGGAAATCAACAATATGGAACACTCTGAAATCAGACTTT 1077  
1021 TAG 1023  
1078 TAG 1080

RESULT 7  
US-09-971-269-6  
; Sequence 6, Application US/09971269  
; Publication No. US20030148281A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Glucksmann, Maria A.  
; TITLE OF INVENTION: 65499 AND 58875, NOVEL SEVEN  
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS AND USES THEREOF  
; FILE REFERENCE: MF100-414P1EM  
; CURRENT APPLICATION NUMBER: US/09/971,269  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/237,700  
; PRIOR FILING DATE: 2000-10-05  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-971-269-6  
Query Match 99.8%; Score 1021.4; DB 10; Length 1023;  
Best Local Similarity 99.9%; Pred No. 0;  
Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAATCCATTTCATGATCTTTGTTGGAACACACCTCTCCGAACTTTTAAACAAATCTCG 60  
DB 1 ATGAATCCATTTCATGATCTTTGTTGGAACACACCTCTCCGAACTTTTAAACAAATCTCG 60  
QY 61 AATAAGAGTTTGGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCTCCCTTCCATG 120  
DB 61 AATAAGAGTTTGGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCTCCCTTCCATG 120  
QY 121 ATTGGGATTTATCTCTTCAACAGGGCTGGTTGGCAACATCTCTCATTTGATTCACATATAA 180  
DB 121 ATTGGGATTTATCTCTTCAACAGGGCTGGTTGGCAACATCTCTCATTTGATTCACATATAA 180  
QY 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTG 240  
DB 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATACCTGCAACCTGGCTGGCTGATTG 240  
QY 241 GTCCACATAGTTGGAATGCTTTTCTTTATTCACCAATGGGCCCGAGGGGAGAGTGGGTG 300  
DB 241 GTCCACATAGTTGGAATGCTTTTCTTTATTCACCAATGGGCCCGAGGGGAGAGTGGGTG 300  
QY 301 TTTGGGGGGCTCTCTGCAACCATCATCACATCCCTGGATCTTTGTAACCAATTTGGCTGT 360  
DB 301 TTTGGGGGGCTCTCTGCAACCATCATCACATCCCTGGATCTTTGTAACCAATTTGGCTGT 360  
QY 361 AGTCCCATCATGACTGTAAATGAGTGTGACAGGTAATTTGCGCTCTGCTCCCAACCAATTCGA 420  
DB 361 AGTCCCATCATGACTGTAAATGAGTGTGACAGGTAATTTGCGCTCTGCTCCCAACCAATTCGA 420  
QY 421 CTGACACCTTTGGAGAACAAAGGTACAAGACCATCCGATCAATTTGGGCCCTTTGGGAGCT 480  
DB 421 CTGACACCTTTGGAGAACAAAGGTACAAGACCATCCGATCAATTTGGGCCCTTTGGGAGCT 480  
QY 481 TCCCTTATCTGAGATTTGCTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 540  
DB 481 TCCCTTATCTGAGATTTGCTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 540  
QY 541 GTTGAGAGTTGCTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 600  
DB 541 GTTGAGAGTTGCTTTGATTTGACATCCCTGACGATGTACTCTGGTATACACTTTAT 600  
QY 601 TTGACGATAACAACTTTTCTTCCCTCTACCTTTGATTTGGTGTGCTATATTTAAAT 660  
DB 601 TTGACGATAACAACTTTTCTTCCCTCTACCTTTGATTTGGTGTGCTATATTTAAAT 660  
QY 661 TTATGCTATATCTGGGAGATGTATCAACAGAAATAAGATGCCAGATGCTGCAATCCCAGT 720  
DB 661 TTATGCTATATCTGGGAGATGTATCAACAGAAATAAGATGCCAGATGCTGCAATCCCAGT 720  
QY 721 GTACCAAAACAGAGAGTGAAGTTCAGAAAGATGGTGTGCTGGTGTAGTCTTT 780  
DB 721 GTACCAAAACAGAGAGTGAAGTTCAGAAAGATGGTGTGCTGGTGTAGTCTTT 780  
QY 781 ATCTGAGTGTGCTGCTTTATCTGATACAACTGGTGAACCTTACAGATGGAACAGCC 840  
DB 781 ATCTGAGTGTGCTGCTTTATCTGATACAACTGGTGAACCTTACAGATGGAACAGCC 840  
QY 841 ACATGGCCTTCTATGTTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC 900  
DB 841 ACATGGCCTTCTATGTTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC 900  
QY 901 ATTAACCTTTTCTTACATCTGCTGAGTGGAAATTTCCAGAAAGCTCTGCTCAAAATC 960  
DB 901 ATTAACCTTTTCTTACATCTGCTGAGTGGAAATTTCCAGAAAGCTCTGCTCAAAATC 960









Matches 1001; Conservative 0; Mismatches 22; Indels 0; Gaps 0;									
QY	1	ATGAATCCATTTTCATGCACTTTTTCGGAACACCTCTGCGCAACTTTTAAACAAATCCTGG	60						
Db	1	ATGAATCCATTTTCATGCACTTTTTCGGAACACCTCTGCGCAACTTTTAAACAAATCCTGG	60						
QY	61	AATAAAGAGTTTCTTATCAAACTGCGAGTGGGTAGATACAGTCACTCTCCCTCCATG	120						
Db	61	AATAAAGAGTTTCTTATCAAACTGCGAGTGGGTAGATACAGTCACTCTCCCTCCATG	120						
QY	121	ATTGGGATATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTTATTAATAATAATA	180						
Db	121	ATTGGGATATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTTATTAATAATAATA	180						
QY	181	AGATCCAGGAAAAAAGTCCCTGATCATCTATATCTGAACCTGCTGCTGCTGATTG	240						
Db	181	AGGTCCAGAAAAAAGTCCCTGATCATCTATATCTGAACCTGCTGCTGCTGATTG	240						
QY	241	GTCCACATAGTTGGAATGCTTTCTTATTCACCAATGGCCCGAGGGGAGAGTGGGTG	300						
Db	241	GTCCACATAGTTGGAATGCTTTCTTATTCACCAATGGCCCGAGGGGAGAGTGGGTG	300						
QY	301	TTTGGGGGCTCTCTGCAACATCATCAATCCCTGATCTTGTAAACCAATTTGCCCTG	360						
Db	301	TTTGGGGGCTCTCTGCAACATCATCAATCCCTGATCTTGTAAACCAATTTGCCCTG	360						
QY	361	AGTCCATATGCTGTAAGTGGTGGAGAGTACTTTGCGCTCTGCTCAACCAATTTGA	420						
Db	361	AGTCCATATGCTGTAAGTGGTGGAGAGTACTTTGCGCTCTGCTCAACCAATTTGA	420						
QY	421	CTGACAGTTGGGAAACAAGTCAAGACCATCCGATCAATTTGGGCTTTGGGAGCT	480						
Db	421	CTGACAGTTGGGAAACAAGTCAAGACCATCCGATCAATTTGGGCTTTGGGAGCT	480						
QY	481	TCCTTTATCTGGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540						
Db	481	TCCTTTATCTGGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540						
QY	541	GTGAGAGTTGGTCTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	600						
Db	541	GTGAGAGTTGGTCTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	600						
QY	601	TTGAGGATTAACAACCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660						
Db	601	TTGAGGATTAACAACCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660						
QY	661	TTATGCTATCTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT	720						
Db	661	TTATGCTATCTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT	720						
QY	721	GTACAAACAGAGAGTGAAGTTGCAAGAATGGTGTGCTGCTGCTGCTGCTGCTGCTT	780						
Db	721	GTACAAACAGAGAGTGAAGTTGCAAGAATGGTGTGCTGCTGCTGCTGCTGCTGCTT	780						
QY	781	ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840						
Db	781	ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840						
QY	841	ACATGCGCTTCTATGTTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC	900						
Db	841	ACATGCGCTTCTATGTTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC	900						
QY	901	ATTAAACCTTTCTTACATCTGCTGAGTGGAAATTTCCAGAAACCTGCTGCTCAATC	960						
Db	901	ATTAAACCTTTCTTACATCTGCTGAGTGGAAATTTCCAGAAACCTGCTGCTCAATC	960						
QY	961	CAAGAAGAGGAGTGTGAGAGGAAATCAACAATATGGAAACACTCTGAAATCACCTTT	1020						
Db	961	CAAGAAGAGGAGTGTGAGAGGAAATCAACAATATGGAAACACTCTGAAATCACCTTT	1020						
QY	1021	TAG 1023							
Db	1021	TAG 1023							

RESULT 13									
US-10-309-515-33									
; Sequence 33, Application US/10309515									
; Publication No. US20030114644A1									
; GENERAL INFORMATION:									
; APPLICANT: Bennett Kinrade, Michele									
; APPLICANT: Brobeck, Robbin M.									
; APPLICANT: Waters, Stephen M.									
; APPLICANT: Krause, James E.									
; TITLE OF INVENTION: Melanin Concentrating Hormone Receptors									
; FILE REFERENCE: N00.2102C1									
; CURRENT APPLICATION NUMBER: US/10/309,515									
; CURRENT FILING DATE: 2002-12-04									
; PRIOR APPLICATION NUMBER: 60/284,835									
; PRIOR FILING DATE: 2001-04-19									
; PRIOR APPLICATION NUMBER: 10/126,764									
; PRIOR FILING DATE: 2002-04-18									
; NUMBER OF SEQ ID NOS: 60									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 33									
; LENGTH: 1023									
; TYPE: DNA									
; ORGANISM: Macaca fascicularis									
US-10-309-515-33									
Query Match 96.2%; Score 984.6; DB 15; Length 1023;									
Best Local Similarity 97.7%; Pred. No. 5.6e-303;									
Matches 999; Conservative 0; Mismatches 24; Indels 0; Gaps 0;									
QY	1	ATGAATCCATTTTCATGCACTTTTTCGGAACACCTCTGCGCAACTTTTAAACAAATCCTGG	60						
Db	1	ATGAATCCATTTTCATGCACTTTTTCGGAACACCTCTGCGCAACTTTTAAACAAATCCTGG	60						
QY	61	AATAAAGAGTTTCTTATCAAACTGCGAGTGGGTAGATACAGTCACTCTCCCTCCATG	120						
Db	61	AATAAAGAGTTTCTTATCAAACTGCGAGTGGGTAGATACAGTCACTCTCCCTCCATG	120						
QY	121	ATTGGGATATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTTATTAATAATAATA	180						
Db	121	ATTGGGATATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTTATTAATAATAATA	180						
QY	181	AGATCCAGGAAAAAAGTCCCTGATCATCTATATCTGAACCTGCTGCTGCTGCTGCTG	240						
Db	181	AGTCCAGAAAAAAGTCCCTGATCATCTATATCTGAACCTGCTGCTGCTGCTGCTG	240						
QY	241	GTCCACATAGTTGGAATGCTTTCTTATTCACCAATGGCCCGAGGGGAGAGTGGGTG	300						
Db	241	GTCCACATAGTTGGAATGCTTTCTTATTCACCAATGGCCCGAGGGGAGAGTGGGTG	300						
QY	301	TTTGGGGGCTCTCTGCAACATCATCAATCCCTGATCTTGTAAACCAATTTGCCCTG	360						
Db	301	TTTGGGGGCTCTCTGCAACATCATCAATCCCTGATCTTGTAAACCAATTTGCCCTG	360						
QY	361	AGTCCATATGCTGTAAGTGGTGGAGAGTACTTTGCGCTCTGCTCAACCAATTTGA	420						
Db	361	AGTCCATATGCTGTAAGTGGTGGAGAGTACTTTGCGCTCTGCTCAACCAATTTGA	420						
QY	421	CTGACAGTTGGGAAACAAGTCAAGACCATCCGATCAATTTGGGCTTTGGGAGCT	480						
Db	421	CTGACAGTTGGGAAACAAGTCAAGACCATCCGATCAATTTGGGCTTTGGGAGCT	480						
QY	481	TCCTTTATCTGGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540						
Db	481	TCCTTTATCTGGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540						
QY	541	GTGAGAGTTGGTCTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	600						
Db	541	GTGAGAGTTGGTCTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	600						
QY	601	TTGAGGATTAACAACCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660						
Db	601	TTGAGGATTAACAACCTTTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660						
QY	661	TTATGCTATCTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT	720						
Db	661	TTATGCTATCTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT	720						
QY	721	GTACAAACAGAGAGTGAAGTTGCAAGAATGGTGTGCTGCTGCTGCTGCTGCTGCTT	780						
Db	721	GTACAAACAGAGAGTGAAGTTGCAAGAATGGTGTGCTGCTGCTGCTGCTGCTGCTT	780						
QY	781	ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840						
Db	781	ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840						
QY	841	ACATGCGCTTCTATGTTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC	900						
Db	841	ACATGCGCTTCTATGTTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC	900						
QY	901	ATTAAACCTTTCTTACATCTGCTGAGTGGAAATTTCCAGAAACCTGCTGCTCAATC	960						
Db	901	ATTAAACCTTTCTTACATCTGCTGAGTGGAAATTTCCAGAAACCTGCTGCTCAATC	960						
QY	961	CAAGAAGAGGAGTGTGAGAGGAAATCAACAATATGGAAACACTCTGAAATCACCTTT	1020						
Db	961	CAAGAAGAGGAGTGTGAGAGGAAATCAACAATATGGAAACACTCTGAAATCACCTTT	1020						
QY	1021	TAG 1023							
Db	1021	TAG 1023							



Db 601 TTGACAAATCAACTTTCTTTTCCCTCTACCTTGATTTGGTGTGCTATATTTTAATT 660  
Qy 661 TTATGCTATCTGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT 720  
Db 661 TTATGCTATCTGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGC 720  
Qy 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGGTGTGCTGGTGTGCTGCTGTTT 780  
Db 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGGTGTGCTGGTGTGCTGCTGTTT 780  
Qy 781 ATCTGAGTCTGCCCTTTATCATGTGATCACTGGTGAATTTACAGATGGAACAGCCC 840  
Db 781 ATCTGAGTCTGCCCTTTATCATGTGATCACTGGTGAATTTACAGATGGAACAGCCC 840  
Qy 841 ACATGCTCTTATGTGGTATTAACCTTCCATCTGCTGATGCTGATGCTGATGCTGATGCT 900  
Db 841 ACATGCTCTTATGTGGTATTAACCTTCCATCTGCTGATGCTGATGCTGATGCTGATGCT 900  
Qy 901 ATTAACCTTTCTCTACATCTGCTGAGTGAATTTCCAGAAAGCTGCTGCTCAATC 960  
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Qy 1021 TAG 1023  
Db 1021 TAG 1023

RESULT 14  
US-10-291-990-1  
; Sequence 1, Application US/10291990  
; Publication No. US20030148457A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett Kinrade, Michele  
; APPLICANT: Brodbeck, Robbin M.  
; APPLICANT: Waters, Stephen  
; APPLICANT: Krause, James E.  
; TITLE OF INVENTION: Monkey and Canine Melanin Concentrating Hormone Receptors  
; FILE REFERENCE: N01.2102  
; CURRENT APPLICATION NUMBER: US/10/291,990  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 60/350,493  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Macaca fascicularis  
US-10-291-990-1

Query Match 96.2%; Score 984.6; DB 15; Length 1023;  
Best Local Similarity 97.7%; Pred. No. 5.6e-303;  
Matches 999; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 ATGAATCCATTTTCATCATCTGTTGGAAACACTCTGCGCACTTTTAAACAAATCTCGG 60  
Db 1 ATGAATCCATTTTCATCATCTGTTGGAAACACTCTGCGCACTTTTAAACAAATCTCGG 60  
Qy 61 AATAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTATCCTCCCTCCATG 120  
Db 61 AATAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTATCCTCCCTCCATG 120  
Qy 121 ATGGGATTTATCTGTTCAACAGGCTGGTGGCAACATCTCTGATTTACTATAATA 180  
Db 121 ATGGGATTTATCTGTTCAACAGGCTGGTGGCAACATCTCTGATTTACTATAATA 180  
Qy 181 AGATCCAGAAAAAACAAGCTGCTGACATCTATATCTGCAACCTGGCTGCTGATTTG 240  
Db 181 AGGTCCAGAAAAAACAAGCTGCTGACATCTATATCTGCAACCTGGCTGCTGATTTG 240

Qy 241 GTCCACATAGTTGGAATGCCCTTTTCTTATTACCAATGGGCCGAGGGAGAGTGGGTG 300  
Db 241 GTCCACATCGTTGGAAATGCCCTTTTCTTATTACCAATGGGCCGAGGGAGAGTGGGTG 300  
Qy 301 TTTGGGGGGCTCTCTGCAACCATCATCATCTGCTGATCTTGTAAACCAATTTGCCCTGT 360  
Db 301 TTTGGGGGGCTCTCTGCAACCATCATCATCTGCTGATCTTGTAAACCAATTTGCCCTGT 360  
Qy 361 AGTGCCATCATGCTGTAATGAGTGTGGACAGGTACTTTGGCCCTGCTCCAAACCAATTTGCA 420  
Db 361 AGTGCCATCATGCTGTAATGAGTGTGGACAGGTACTTTGGCCCTGCTCCAAACCAATTTGCA 420  
Qy 421 CTGACACCTTTGGAGAAACAGGTAACAAGCAATCCGATCAATTTGGGCTTTTGGGAGCT 480  
Db 421 CTGACAGTGTGGAGAAACAGGTAACAAGCAATCCGATCAATTTGGGCTTTTGGGAGCT 480  
Qy 481 TCCCTTATCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 TCCCTTATCTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Qy 541 GTTGAGAGTGTGCTTTTGTATTTGACATCCCTGACGATGCTGCTGCTGCTGCTGCTGCTGCT 600  
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Qy 601 TTGACGATAACAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660  
Db 601 TTGACGATAACAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660  
Qy 661 TTATGCTATCTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCCAGT 720  
Db 661 TTATGCTATCTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCCAGC 720  
Qy 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 GTACCAAAACAGAGATGATGAAGTTGACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Db 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Qy 841 ACATGCTGCTTCTATGTTGGTATTTAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 ACATGCTGCTTCTATGTTGGTATTTAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 901 ATTAACCTTTCTCTACATCTGCTGAGTGAATTTCCAGAAAGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 ATTAACCTTTCTCTACATCTGCTGAGTGAATTTCCAGAAAGCTGCTGCTGCTGCTGCTGCT 960  
Qy 961 CAAAGAGAGCGCTGAGAGGAAATCAACAATATGGGAAACACTCTGCAATCACACTTT 1020  
Db 961 CAAAGAGAGTGAAGTGAAGGAAATCAAAAATATGGGAAACACTCTGCAATCACACTTT 1020  
Qy 1021 TAG 1023  
Db 1021 TAG 1023

RESULT 15  
US-10-126-764-33  
; Sequence 33, Application US/10126764  
; Publication No. US20030166834A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett Kinrade, Michele  
; APPLICANT: Brodbeck, Robbin  
; APPLICANT: Krause, James  
; TITLE OF INVENTION: MELANIN CONCENTRATING HORMONE RECEPTORS  
; FILE REFERENCE: N00.2102  
; CURRENT APPLICATION NUMBER: US/10/126,764  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: 60/284,835  
; PRIOR FILING DATE: 2001-04-19  
; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Macaca fascicularis  
US-10-126-764-33

Query Match 96.2%; Score 984.6; DB 15; Length 1023;  
Best Local Similarity 97.7%; Pred. No. 5.6e-303;  
Matches 999; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY	1	ATGATCCATTTTCATGCTGTTGGACACCTCTGCGAACTTTTAAACAAATCCCTGG	60
DB	1	ATGATCCATTTTCATGCTGTTGGACACCTCTGCGAACTTTTAAACAAATCCCTGG	60
QY	61	AATAAGAGTTTGTCTATCAAAATGCGAGTGGTAGATACAGTCATCCCTCCCTCCATG	120
DB	61	AATAAGAGTTTGTCTATCAAAATGCGAGTGGTAGATACAGTCATCCCTCCCTCCATG	120
QY	121	ATTGGGATTATCTGTTCAACAGGGCTGTTGGCAACATCTCTATTGTTTACTATAATA	180
DB	121	ATTGGGATTATCTGTTCAACAGGGCTGTTGGCAACATCTCTATTGTTTACTATAATA	180
QY	181	AGATCCAGGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTATTG	240
DB	181	AGGTCAGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTATTG	240
QY	241	GTCCACATAGTTGAATGCCCTTTTCTATTACCAATGGSCCGAGGGGAGAGTGGTG	300
DB	241	GTCCACATAGTTGAATGCCCTTTTCTATTACCAATGGSCCGAGGGGAGAGTGGTG	300
QY	301	TTTGGGGGGCTCTCTGCAACATCATCATCTCTGATCTTGTAAACCAATTTGCTGT	360
DB	301	TTTGGGGGGCTCTCTGCAACATCATCATCTCTGATCTTGTAAACCAATTTGCTGT	360
QY	361	AGTCCCATATGATGTAATGAGTGGACAGTACTTTGCCCTCTGTCACCAATTTTGA	420
DB	361	AGTCCCATATGATGTAATGAGTGGACAGTACTTTGCCCTCTGTCACCAATTTTGA	420
QY	421	CTGACAGTGGGAGACAAAGTACAGACCATCCGATCAATTTGGGCGAGCT	480
DB	421	CTGACAGTGGGAGACAAAGTACAGACCATCCGATCAATTTGGGCGAGCT	480
QY	481	TCCTTTATCTGGCATTCCTGCTGGTCTACTCGAAGGTCTCAAAATTTAAAGACGT	540
DB	481	TCCTTTATCTGGCATTCCTGCTGGTCTACTCGAAGGTCTCAAAATTTAAAGACGT	540
QY	541	GTGAGAGTTGTGCTTTTGTGATTTGACATCCCTGACGATGCTGCTGATACACTTAT	600
DB	541	GTGAGAGTTGTGCTTTTGTGATTTGACATCCCTGACGATGCTGCTGATACACTTAT	600
QY	601	TTGACGATTAACACTTTTTCCTCTACCTTTCATTTGGTGTGCTATATTTAAAT	660
DB	601	TTGACGATTAACACTTTTTCCTCTACCTTTCATTTGGTGTGCTATATTTAAAT	660
QY	661	TTATGCTATATCTGGGAGATGATCAACAGAAATAGGATCCAGATGCTGCAATCCAGT	720
DB	661	TTATGCTATATCTGGGAGATGATCAACAGAAATAGGATCCAGATGCTGCAATCCAGC	720
QY	721	GTACCAAAACAGAGAGTGAAGTTCACAAAGATGGTGTGCTGCTGGTGTAGTCTTT	780
DB	721	GTACCAAAACAGAGAGTGAAGTTCACAAAGATGGTGTGCTGCTGGTGTAGTCTTT	780
QY	781	ATCTGAGTGTGCCCTTATCATGTGATACAACTGGTGAATTAAGATGGAACAGCCC	840
DB	781	ATCTGAGTGTGCCCTTATCATGTGATACAACTGGTGAATTAAGATGGAACAGCCC	840
QY	841	ACACTGGCTTCTATGTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC	900
DB	841	ACACTGGCTTCTATGTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC	900
QY	901	ATTAACCCCTTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCCTCAATC	960
DB	901	ATTAACCCCTTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCCTCAATC	960

DB	901	ATTAACCCCTTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAACGTCTGCCCTCAATC	960
QY	961	CAAGAAGAGCGACTGAGAGGAATCAACAATATGGAAACACTCTGAAATCACACTTT	1020
DB	961	CAAGAAGAGCGACTGAGAGGAATCAACAATATGGAAACACTCTGAAATCACACTTT	1020
QY	1021	TAG 1023	
DB	1021	TAG 1023	

Search completed: May 17, 2004, 23:56:05  
Job time : 506 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 13:07:12 ; Search time 471 Seconds  
(without alignments)  
9226.978 Million cell updates/sec

Title: US-09-913-770B-2  
Perfect score: 1023  
Sequence: 1 atgaatccatttcgcatc.....ctctgaatcacacttttag 1023

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1023	100.0	1023	4	Aaf85372 Nucleotid
3	1023	100.0	1023	5	Aai171927 Human mel
4	1023	100.0	1023	5	Aas07954 Human CDN
5	1023	100.0	1023	6	Abk10852 CDNA enco
6	1023	100.0	1023	6	Abk86285 Human TGR
7	1023	100.0	1023	7	Aad36796 Human mel
8	1023	100.0	1023	7	Aad54241 Human mel
9	1023	100.0	1023	8	Aal57671 Human mel
10	1023	100.0	1023	9	Aad51085 Human G P
11	1023	100.0	1035	6	Abk10848 DNA enco
12	1023	100.0	1965	4	AAS42862 Human G P
13	1021.4	99.8	1023	5	Aaf58619 Human AXO
14	1021.4	99.8	1023	6	Abk141166 Human sev
15	1021.4	99.8	1278	6	Abk141165 Human sev
16	1021	99.8	1330	7	Abz42591 Human G P
17	987.8	96.6	1023	9	Aad62476 Monkey MC
18	986.2	96.4	1075	5	Ade24770 Monkey MC
19	984.6	96.2	1023	5	Aai171932 Human mel
20	984.6	96.2	1023	7	Aad48422 Rhesus mo
21	984.6	96.2	1023	9	Aad62474 Monkey MC
22	983.2	96.1	1020	9	Ade24775 Monkey me
23	983	96.1	1023	9	Aad62475 Monkey MC

24	981.4	95.9	1558	6	AAD29677	Aad29677 Human G-p
25	887	86.7	1023	7	AAD48421	Aad48421 Ferrret MC
26	887	86.7	1023	7	AAD48423	Aad48423 Human MCH
27	869.4	85.0	1023	9	ADE24771	Ade24771 Cat MCH r
28	866.4	84.7	1020	9	ADE24745	Ade24745 Cat melan
29	846.6	82.8	1021	9	ADE24772	Ade24772 Dog MCH r
30	834.6	81.6	990	9	ADE24755	Ade24755 Dog melan
31	834.6	81.6	993	9	AAD62477	Aad62477 Canine MC
32	831	81.2	993	7	AAD48420	Aad48420 Dog MCH-2
33	716	70.0	757	6	ABK10849	Abk10849 G protein
34	484.2	47.3	546	5	AAF93609	Aaf93609 cDNA isol
35	473.6	46.3	954	9	ADC12691	Adc12691 Human GPC
36	458.2	44.8	863	7	ABZ36066	Abz36066 Human sec
37	368.8	36.1	983	9	ADE24739	Ade24739 Cat melan
38	306.2	29.9	679	4	AAS42844	Aas42844 Human G P
39	270.6	26.5	431	9	ADE24742	Ade24742 Cat melan
40	248	24.2	386	3	AAC03164	Aac03164 Human sec
41	230.2	22.5	1080	9	AAD62483	Aad62483 Monkey MC
42	216.6	21.2	1044	9	AAD62489	Aad62489 Monkey MC
43	215.4	21.1	735	4	AAS42937	Aas42937 DNA enco
44	215.4	21.1	925	4	Aaf85373	Aaf85373 Nucleotid
45	201.6	19.7	300	9	ADE24752	Ade24752 Dog melan

ALIGNMENTS

RESULT 1

AAA90097  
ID AAA90097 standard; DNA; 1023 BP.

XX  
AC AAA90097;

XX  
DT 02-JAN-2001 (first entry)

XX  
DE Human G-protein coupled receptor SLT encoding DNA sequence.

XX  
KW G-protein coupled receptor; SLT; antiallergic; antirheumatic;  
antidiabetic; nootropic; neuroprotective; antiinflammatory; neuroleptic;  
hypotensive; nervous system disorder; hormonal disorder; schizophrenia;  
inflammatory diseases; cardiovascular disease; Alzheimer's disease;  
allergy; rheumatism; sodium intolerance; diabetes; hypertension; ds.

XX  
OS Homo sapiens.

XX  
PN WO200049046-A1.

XX  
PD 24-AUG-2000.

XX  
PF 18-FEB-2000; 2000WO-JP000927.

XX  
PR 19-FEB-1999; 99JP-00041336.

XX  
PR 06-MAY-1999; 99JP-00125768.

XX  
(TAKE ) TAKEDA CHEM IND LTD.

XX  
Watanabe T, Terao Y, Shintani Y;

XX  
WPI: 2000-543749/49.

XX  
P-PSDB; AAB23540.

XX  
G protein coupled receptor protein SLT, DNA encoding it and antibodies  
recognizing it, useful for treatment and diagnosis of e.g. neurological  
diseases.

XX  
Claim 5; Fig 1; 108pp; Japanese.

XX  
This invention relates to a G-protein coupled receptor protein, SLT of  
human origin. The nucleotide and protein sequences are given in the  
specification. The invention includes expression vector containing SLT  
encoding polynucleotide sequences, host cells transformed with the  
vectors, and methods for preparing SLT through the culturing of the  
transformants. Also included are anti-SLT antibodies, SLT ligands and

CC methods for their identification. SLT exhibits antiallergic,  
CC antihistaminic, antidiabetic, nootropic, neuroprotective,  
CC antiinflammatory, neuroleptic, and hypotensive activity. The G protein  
CC coupled receptor protein SLT, the DNA encoding it and its antibodies can  
CC be used for the diagnosis and treatment of diseases with which SLT is  
CC associated, such as disorders of SLT expression. These include nervous  
CC system disorders, hormonal disorders, inflammatory diseases, (such  
CC cardiovascular diseases, and liver/gall bladder/pancreas diseases, (such  
CC as Alzheimer's disease, schizophrenia, allergies, rheumatism, sodium  
CC intolerance, diabetes and hypertension). The present sequence represents  
CC the SLT DNA sequence of the invention  
XX  
SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 3; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 1.8e-295;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATCCATTTCATGTCATCTTGTGGAACACCTCTGCGAACCTTTTAAACAAATCCTGG 60  
DB 1 ATGATCCATTTCATGTCATCTTGTGGAACACCTCTGCGAACCTTTTAAACAAATCCTGG 60  
QY 61 AATAAGAGTTTGGTTATCAAACTGCCAGTGTGGTAGATACAGTCACTCCTCCCTCCATG 120  
DB 61 AATAAGAGTTTGGTTATCAAACTGCCAGTGTGGTAGATACAGTCACTCCTCCCTCCATG 120  
QY 121 ATTGGGATTAATCTGTTCAACAGGGCTGTTGGCAACATCCTCATCTATTCTACTATAATA 180  
DB 121 ATTGGGATTAATCTGTTCAACAGGGCTGTTGGCAACATCCTCATCTATTCTACTATAATA 180  
QY 181 AGATCCAGGAAAAAAGAGTCCCTGACATCTATCTGCAACCTGCTGTGCTGATTTG 240  
DB 181 AGATCCAGGAAAAAAGAGTCCCTGACATCTATCTGCAACCTGCTGTGCTGATTTG 240  
QY 241 GTCCACATAGTTGAATGCTTTCTTATTCACAAATGGGCCCGAGGGAGAGTGGTG 300  
DB 241 GTCCACATAGTTGAATGCTTTCTTATTCACAAATGGGCCCGAGGGAGAGTGGTG 300  
QY 301 TTTGGGGGGCTCTCTGCACATCATCAGTCTGATCTTGTAAACAAATTTGCTCTGT 360  
DB 301 TTTGGGGGGCTCTCTGCACATCATCAGTCTGATCTTGTAAACAAATTTGCTCTGT 360  
QY 361 AGTGCCATCATGCTGTAATGAGTGTGGACAGTACTTTGCCCTCGTCCAAACCATTTGCA 420  
DB 361 AGTGCCATCATGCTGTAATGAGTGTGGACAGTACTTTGCCCTCGTCCAAACCATTTGCA 420  
QY 421 CTGACAGCTTGGAGAACAGGTACAGACCATCGGATCAATTTGGGCCCTTTGGGCGAGT 480  
DB 421 CTGACAGCTTGGAGAACAGGTACAGACCATCGGATCAATTTGGGCCCTTTGGGCGAGT 480  
QY 481 TCCTTTATCCTGGCAATGCTGCTGCTGCTCTACTCGAAGGTCTCAAAATTTAAAGACGGT 540  
DB 481 TCCTTTATCCTGGCAATGCTGCTGCTGCTCTACTCGAAGGTCTCAAAATTTAAAGACGGT 540  
QY 541 GTTGAGAGTTGTGCTTTGATTTGACATCCCTTGAAGATGCTGCTGCTGCTGCTGCTTAT 600  
DB 541 GTTGAGAGTTGTGCTTTGATTTGACATCCCTTGAAGATGCTGCTGCTGCTGCTGCTTAT 600  
QY 601 TTGACGATTAACAATTTTTTTTCCCTTACCTTGAATTTGGTGTGCTATATTTAAAT 660  
DB 601 TTGACGATTAACAATTTTTTTTCCCTTACCTTGAATTTGGTGTGCTATATTTAAAT 660  
QY 661 TTATGCTATATCTGGGAGATGATCAACAGAAATGAAGATGCCAGATGCTGCAATCCAGT 720  
DB 661 TTATGCTATATCTGGGAGATGATCAACAGAAATGAAGATGCCAGATGCTGCAATCCAGT 720  
QY 721 GTACCAAAACAGAGTGAAGTCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTT 780  
DB 721 GTACCAAAACAGAGTGAAGTCAACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTT 780  
QY 781 ATCTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
DB 781 ATCTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

QY 841 ACATGGCCCTTCTATCTATGTTGGTTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC 900  
DB 841 ACATGGCCCTTCTATCTATGTTGGTTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGC 900  
QY 901 ATTAACCCCTTTCTCTACATCTCTGCTGAGTGGAAATTTCCAGAAACGCTTGCCTCAAATC 960  
DB 901 ATTAACCCCTTTCTCTACATCTCTGCTGAGTGGAAATTTCCAGAAACGCTTGCCTCAAATC 960  
QY 961 CAAGAAGAGGAGTGAAGAGAAATCAACATATGGAACACTCTGAATCAGACTTT 1020  
DB 961 CAAGAAGAGGAGTGAAGAGAAATCAACATATGGAACACTCTGAATCAGACTTT 1020  
QY 1021 TAG 1023  
DB 1021 TAG 1023  
RESULT 2  
ID AAF85372 standard; DNA; 1023 BP.  
XX AAF85372;  
AC AAF85372;  
DT 23-JUL-2001 (first entry)  
XX Nucleotide sequence of human G-protein coupled receptor HG67.  
DE G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress;  
KW melanin concentrating hormone receptor; cancer; pain; sexual dysfunction;  
KW weight gain; hypertension; dyslipidemia; cardiovascular disease;  
KW gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;  
KW cachexia; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1..1023  
FT /tag= .a  
FT /product= "G-protein coupled receptor HG67"  
XX \*WO200136479-A1.  
XX 25-MAY-2001.  
XX 14-NOV-2000; 2000WO-US031240.  
XX 16-NOV-1999; 99US-0165871P.  
PR 13-MAR-2000; 2000US-0188977P.  
PR 18-APR-2000; 2000US-0198029P.  
XX (MERI ) MERCK & CO INC.  
PA (BANY ) BANYU PHARM CO LTD.  
XX Liu Q, McDonald TP, Howard AD, Iwaasa H, Sano H;  
WPI; 2001-355618/37.  
P-PSDB; AAB68428.  
XX New G-protein coupled receptor, designated MCH-R2, is a receptor for  
PT melanin-concentrating hormone and is useful to provide treatment for  
PT weight disorders including obesity.  
XX Claim 7; Page 25-26; 32pp; English.  
XX The present sequence encodes a human G-protein coupled receptor,  
CC designated HG67 or MCH-R2. HG67 is a melanin concentrating hormone  
CC receptor. Modulators of HG67 can be used to treat a patient, particularly  
CC to reduce weight, particularly in obesity, or to treat stress. These  
CC modulators can also be used to treat cancer, reduce pain, treat sexual  
CC dysfunction or to produce weight gain. Bringing about weight loss can be  
CC used to reduce the likelihood of hypertension, diabetes, dyslipidemia,  
CC cardiovascular disease, gall stones, osteoarthritis or certain forms of

CC cancers. Increasing weight can be useful in the treatment of anorexia.  
CC AIDS, wasting, cachexia and frail elderly patients, or those undergoing  
CC chemotherapy or radiation therapy  
XX  
SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1023; DB 4; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 1.8e-295;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATCATTTTCATGCACTTTGTTGGAACACCTCTGCCGAACCTTTTAAACAAATCCTGG 60  
DB 1 ATGAATCATTTTCATGCACTTTGTTGGAACACCTCTGCCGAACCTTTTAAACAAATCCTGG 60  
QY 61 AATAAGAGTTTGTCTTATCAAACTCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 120  
DB 61 AATAAGAGTTTGTCTTATCAAACTCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 120  
QY 121 ATTGGATTATCTGTTCAACAGGGTGGTTGGCAACATCTCTCATTTGTTTACATATAATA 180  
DB 121 ATTGGATTATCTGTTCAACAGGGTGGTTGGCAACATCTCTCATTTGTTTACATATAATA 180  
QY 181 AGATCCAGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240  
DB 181 AGATCCAGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTG 240  
QY 241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300  
DB 241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300  
QY 301 TTTGGGGGCTCTCTGCAACCATCATACATCCCTGGATACCTTTGTAACCAATTTGCCCTGT 360  
DB 301 TTTGGGGGCTCTCTGCAACCATCATACATCCCTGGATACCTTTGTAACCAATTTGCCCTGT 360  
QY 361 AGTGCCATCATGACTGTAATGAGTGTGGACAGTACTTTGCCCTCTGTCACCACTTTTGA 420  
DB 361 AGTGCCATCATGACTGTAATGAGTGTGGACAGTACTTTGCCCTCTGTCACCACTTTTGA 420  
QY 421 CTGACACGTTGGAGAACAGGTACAGACCATCCCGATCAATTTGGGCTTTGGGACGCT 480  
DB 421 CTGACACGTTGGAGAACAGGTACAGACCATCCCGATCAATTTGGGCTTTGGGACGCT 480  
QY 481 TCCTTTATCTGGCATGCTCTCTGCTGGTGTACTCGMAGGTATCAATTAATTAAGACGCT 540  
DB 481 TCCTTTATCTGGCATGCTCTCTGCTGGTGTACTCGMAGGTATCAATTAATTAAGACGCT 540  
QY 541 GTTGAGAGTTGTGCTTTTGTGATTTGATCTCCCTGACGATGTACTCTGTTATACACTTTAT 600  
DB 541 GTTGAGAGTTGTGCTTTTGTGATTTGATCTCCCTGACGATGTACTCTGTTATACACTTTAT 600  
QY 601 TTGACGATAACAACTTTTCTTCTTCCCTCTACCCCTTGANTTTGGTGTGCTATATTTAAT 660  
DB 601 TTGACGATAACAACTTTTCTTCTTCCCTCTACCCCTTGANTTTGGTGTGCTATATTTAAT 660  
QY 661 TTATGCTATCTTGGAGATGTATCAACAGATAGGATGCGAGATGCTGCAATCCCACT 720  
DB 661 TTATGCTATCTTGGAGATGTATCAACAGATAGGATGCGAGATGCTGCAATCCCACT 720  
QY 721 GTACCAAAAACAGAGAGTGTAGTGAAGTTGACAAAGATGGTCTGGTCTGCTGTAGTCTTT 780  
DB 721 GTACCAAAAACAGAGAGTGTAGTGAAGTTGACAAAGATGGTCTGGTCTGCTGTAGTCTTT 780  
QY 781 ATCTTGAGTGTGCTGCTTATCATGTGATACAACTGGTGAACCTTACAGTGAACAGGCC 840  
DB 781 ATCTTGAGTGTGCTGCTTATCATGTGATACAACTGGTGAACCTTACAGTGAACAGGCC 840  
QY 841 ACACTGGCTTCTATGTGGTGTATTTACCTCTCCATCTGCTCTGCTATGCGACAGCAGC 900  
DB 841 ACACTGGCTTCTATGTGGTGTATTTACCTCTCCATCTGCTCTGCTATGCGACAGCAGC 900  
QY 901 ATTAACCCCTTTCTCTACATCTGCTGAGTGAATTTCCAGAAACGCTGTGCTCAATC 960  
DB 901 ATTAACCCCTTTCTCTACATCTGCTGAGTGAATTTCCAGAAACGCTGTGCTCAATC 960

QY 961 CAAGAAGACGAGTCTGAGAAGGAAATCAACAATATGGGAACACTCTGAAATCACACTTT 1020  
DB 961 CAAGAAGACGAGTCTGAGAAGGAAATCAACAATATGGGAACACTCTGAAATCACACTTT 1020  
QY 1021 TAG 1023  
DB 1021 TAG 1023  
RESULT 3  
AAI71927  
ID AAI71927 standard; cDNA; 1023 BP.  
XX  
AC AAI71927;  
XX  
DT 16-JAN-2002 (first entry)  
XX  
DE Human melanin concentrating hormone receptor coding sequence #1.  
XX  
KW Human; melanin concentrating hormone; MCH; MCH receptor;  
KW G protein coupled receptor; obesity; cachexia; anorexia nervosa;  
KW hyperphagia; anorectic; antianorectic; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..1023  
FT /\*tag= a  
FT /product= "human melanin concentrating hormone receptor"  
XX  
XX WO200170975-A1.  
XX 27-SEP-2001.  
XX 23-MAR-2001; 2001WO-JP002343.  
XX 24-MAR-2000; 2000JP-00088588.  
XX (YAMA) YAMANOUCHI PHARM CO LTD.  
XX (HELI-) HELIX RES INST.  
XX Kurama T, Matsumoto S, Takasaki J, Matsumoto M, Kamohara M;  
XX Saito T, Oda T, Saito Y;  
XX WPI; 2001-639126/73.  
XX P-PSDB; AAM51567.  
XX New protein with melanin concentrating hormone receptor activity, for  
XX finding antagonists for treating obesity and eating disorders.  
XX Claim 3; Page 47; 62pp; Japanese.  
XX The invention relates to a novel protein comprising a fully defined 340  
XX amino acid sequence, or the sequence containing one or more amino acid  
XX substitutions, deletions or insertions. The protein shows melanin  
XX concentrating hormone (MCH) receptor activity. It is a G protein coupled  
XX receptor that binds to MCH. The protein is used to find agents to treat  
XX obesity, cachexia, anorexia nervosa and hyperphagia. The present sequence  
XX encodes the protein of the invention  
SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1023; DB 5; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 1.8e-295;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATCCATTTTCATGCACTTTGTTGGAACACCTCTGCCGAACCTTTTAAACAAATCCTGG 60  
DB 1 ATGAATCCATTTTCATGCACTTTGTTGGAACACCTCTGCCGAACCTTTTAAACAAATCCTGG 60  
QY 61 AATAAGAGTTTGTCTTATCAAACTCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 120  
DB 61 AATAAGAGTTTGTCTTATCAAACTCCAGTGTGGTAGATACAGTCACTCTCCCTCCCATG 120

Db 61 AATAAAGAGTTTGTCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTCCATG 120  
Qy 121 ATTGGGATATCTGTTCAACAGGGCTGGTGGCAACATCCTCATCTATCTACTATAATA 180  
Db 121 ATTGGGATATCTGTTCAACAGGGCTGGTGGCAACATCCTCATCTATCTACTATAATA 180  
Qy 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGCTGATTG 240  
Db 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGCTGATTG 240  
Qy 241 GTCCACATAGTTGGAATGCTTTCTTATCACCATGCGCCGAGGGGAGAGTGGGTG 300  
Db 241 GTCCACATAGTTGGAATGCTTTCTTATCACCATGCGCCGAGGGGAGAGTGGGTG 300  
Qy 301 TTTGGGGGGCTCTCTGCAACATCATCATCCTCGTACTGTAAACAAATTTGCTCTGT 360  
Db 301 TTTGGGGGGCTCTCTGCAACATCATCATCCTCGTACTGTAAACAAATTTGCTCTGT 360  
Qy 361 AGTGCCATCATGACTGTATAGTGTGGACAGTACTTTTGCCTCTGTCACCAATTTGCA 420  
Db 361 AGTGCCATCATGACTGTATAGTGTGGACAGTACTTTTGCCTCTGTCACCAATTTGCA 420  
Qy 421 CTGACAGTTGGAGAACAGGTACAGACCATCCGATCAATTTGGGCTTTGGGCGAGT 480  
Db 421 CTGACAGTTGGAGAACAGGTACAGACCATCCGATCAATTTGGGCTTTGGGCGAGT 480  
Qy 481 TCCTTTATCTGTCATTTGCTGTCTGGGCTACTCGAAGTCAATCAAAATTTAAAGACGT 540  
Db 481 TCCTTTATCTGTCATTTGCTGTCTGGGCTACTCGAAGTCAATCAAAATTTAAAGACGT 540  
Qy 541 GTTGAGAGTTGCTTTTGAATTTGATCCCTGACGATGTACTCTGTGTATACATTTAT 600  
Db 541 GTTGAGAGTTGCTTTTGAATTTGATCCCTGACGATGTACTCTGTGTATACATTTAT 600  
Qy 601 TTGACGATAACAATTTTTTTTCCCTCTACCTCTGATTTTGGTGTCTATATTTAAT 660  
Db 601 TTGACGATAACAATTTTTTTTCCCTCTACCTCTGATTTTGGTGTCTATATTTAAT 660  
Qy 661 TTATGCTATCTTGGGAGATGTATCAACAGATTAAGGATGCCAGATGCTGCAATCCAGT 720  
Db 661 TTATGCTATCTTGGGAGATGTATCAACAGATTAAGGATGCCAGATGCTGCAATCCAGT 720  
Qy 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGCTGCTGGTGTGCTGTCTTT 780  
Db 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGCTGCTGGTGTGCTGTCTTT 780  
Qy 781 ATCCTGAGTGTGCTCCCTTATCATATGATGATACAACTGGTGAATACAGATGAACGCC 840  
Db 781 ATCCTGAGTGTGCTCCCTTATCATGTGATACAACTGGTGAATACAGATGAACGCC 840  
Qy 841 ACACCTGCTTCTATGCTGGGTATTAACCTCTCATCTGCTCAGCTATGCCAGCAGC 900  
Db 841 ACACCTGCTTCTATGCTGGGTATTAACCTCTCATCTGCTCAGCTATGCCAGCAGC 900  
Qy 901 ATTAACCTTTTCTTACATCTCTGCTGAGTGAATTTCCAGAAAGCTGCTCCTCAATC 960  
Db 901 ATTAACCTTTTCTTACATCTCTGCTGAGTGAATTTCCAGAAAGCTGCTCCTCAATC 960  
Qy 961 CAAGAAGAGCGACTGAGAGGAAATCAACATATGGGAAACACTCTGAATCACTTT 1020  
Db 961 CAAGAAGAGCGACTGAGAGGAAATCAACATATGGGAAACACTCTGAATCACTTT 1020  
Qy 1021 TAG 1023  
Db 1021 TAG 1023

RESULT 4  
AAS07954  
ID AAS07954 standard; cDNA; 1023 BP.  
XX AC  
XX AAS07954;

DT XX 23-OCT-2001 (first entry)  
DE XX Human cDNA encoding G-protein coupled receptor, hRUP27.  
XX  
KW Human; G-protein coupled receptor; GPCR; hRUP27; agonist;  
XX inverse agonist; lung cancer; ss.  
OS XX Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 1: 1023  
FT /\*tag= a  
FT /product= "hRUP27"  
XX  
PN WO200136471-A2.  
PD 25-MAY-2001.  
XX  
PF 16-NOV-2000; 2000WO-US031509.  
XX  
PR 17-NOV-1999; 99US-0166088P.  
PR 17-NOV-1999; 99US-0166099P.  
PR 23-NOV-1999; 99US-0166369P.  
PR 23-DEC-1999; 99US-0171900P.  
PR 23-DEC-1999; 99US-0171901P.  
PR 23-DEC-1999; 99US-0171902P.  
PR 11-FEB-2000; 2000US-0181749P.  
PR 14-MAR-2000; 2000US-0189258P.  
PR 14-MAR-2000; 2000US-0189259P.  
PR 10-APR-2000; 2000US-0195898P.  
PR 10-APR-2000; 2000US-0195899P.  
PR 10-APR-2000; 2000US-0196078P.  
PR 28-APR-2000; 2000US-0200419P.  
PR 12-MAY-2000; 2000US-0203630P.  
PR 12-JUN-2000; 2000US-0210741P.  
PR 12-JUN-2000; 2000US-0210982P.  
PR 21-AUG-2000; 2000US-0226760P.  
PR 26-SEP-2000; 2000US-0235418P.  
PR 26-SEP-2000; 2000US-0235779P.  
PR 20-OCT-2000; 2000US-0242332P.  
PR 20-OCT-2000; 2000US-0242343P.  
PR 24-OCT-2000; 2000US-0243019P.  
XX  
PA (AREN-) ARENA PHARM INC.  
XX  
PI Chen R, Dang HT, Lowitz KP;  
XX  
XX WPI; 2001-355616/37.  
DR P-PSDB; AAU04381.  
XX  
PT Endogenous and non-endogenous versions of human G-protein coupled  
PT receptors for direct identification of candidate compounds as agonists,  
PT inverse agonists or partial agonists for use as therapeutic agents.  
XX  
PS Claim 79; Page 124-125; 160pp; English.  
XX  
XX The sequence encodes a human G-protein coupled receptor (GPCR), hRUP27.  
XX The endogenous and non-endogenous, constitutively activated versions of  
XX human G-protein coupled receptors (GPCR), are useful for direct  
XX identification of candidate compounds as receptor agonists, inverse  
XX agonists or partial agonists having applicability as therapeutic agents  
XX for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous  
XX version of human GPCRs are also utilized in research settings and in  
XX vitro and in vivo system, incorporating GPCRs can be utilised to  
XX elucidate and understand the roles these receptors play in the human  
XX condition, both normal and diseased  
XX  
SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 5; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 1.8e-295;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAATCCATTTCATGCACTCTTTGGGAACACCTCTGCCGAACCTTTTAAACAAATCTCTGG 60
DB |||
1 ATGAATCCATTTCATGCACTCTTTGGGAACACCTCTGCCGAACCTTTTAAACAAATCTCTGG 60
QY 61 AATAAAGAGTTTGGCTTATCAAACTCCAGTGTGGTAGATACAGTCATCTCCCTCCATG 120
DB |||
61 AATAAAGAGTTTGGCTTATCAAACTCCAGTGTGGTAGATACAGTCATCTCCCTCCATG 120
QY 121 ATGGGATTATCTGTTCACAGGCTGTGTGGCAACATCTCTCATCTGTTTACATTAATA 180
DB |||
121 ATGGGATTATCTGTTCACAGGCTGTGTGGCAACATCTCTCATCTGTTTACATTAATA 180
QY 181 AGATCCAGGAAACAAACAGTCCCTGACATCTATCTCAACCTGGCTGGCTGATTG 240
DB |||
181 AGATCCAGGAAACAAACAGTCCCTGACATCTATCTCAACCTGGCTGGCTGATTG 240
QY 241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCCGAGGGAGAGTGGTG 300
DB |||
241 GTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCCGAGGGAGAGTGGTG 300
QY 301 TTTGGGGGCTCTCTGCACCATCATCATCCCTGGATCTTGTAAACAAATTTGCCGT 360
DB |||
301 TTTGGGGGCTCTCTGCACCATCATCATCCCTGGATCTTGTAAACAAATTTGCCGT 360
QY 361 AGTGCCATCATCTGTATAGTGTGACAGGTACTTTGCCCTCGTCCAAACCATTTCCA 420
DB |||
361 AGTGCCATCATCTGTATAGTGTGACAGGTACTTTGCCCTCGTCCAAACCATTTCCA 420
QY 421 CTGACACGTTGGAGAACAGGTACAGACCATCCGATCAATTTGGGCTTTGGGCGACT 480
DB |||
421 CTGACACGTTGGAGAACAGGTACAGACCATCCGATCAATTTGGGCTTTGGGCGACT 480
QY 481 TCCCTTATCCCTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB |||
481 TCCCTTATCCCTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GTTGAGAGTTGTGCTTTTGAATTTGACATCCCTGACGATGTACTCTGTTATACACTTTAT 600
DB |||
541 GTTGAGAGTTGTGCTTTTGAATTTGACATCCCTGACGATGTACTCTGTTATACACTTTAT 600
QY 601 TTGACGATTAACACTTTTTCCTCTACCTCTGATTTGGTGTCTATATTTAAT 660
DB |||
601 TTGACGATTAACACTTTTTCCTCTACCTCTGATTTGGTGTCTATATTTAAT 660
QY 661 TTATGCTATCTTGGAGATGTATCAACAGATTAAGGATGCCAGATGCTGCAATCCCACT 720
DB |||
661 TTATGCTATCTTGGAGATGTATCAACAGATTAAGGATGCCAGATGCTGCAATCCCACT 720
QY 721 GTACCAAAAACAGAGATGTAGAGTTGACAAAGATGGTCTGCTGCTGCTGCTGCTGCTTT 780
DB |||
721 GTACCAAAAACAGAGATGTAGAGTTGACAAAGATGGTCTGCTGCTGCTGCTGCTGCTTT 780
QY 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB |||
781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 ACACCTGCTCTTATGTTGGTTTATACCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB |||
841 ACACCTGCTCTTATGTTGGTTTATACCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 AATAACCTTTCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB |||
901 AATAACCTTTCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 CAAAGAGAGCGACTGAGAGGAAATCAACATATGAGGAAACACTCTGAAATCAACACTTT 1020
DB |||
961 CAAAGAGAGCGACTGAGAGGAAATCAACATATGAGGAAACACTCTGAAATCAACACTTT 1020
QY 1021 TAG 1023
DB |||
1021 TAG 1023
```

```
RESULT 5
ABK10852
ID ABK10852 standard; cDNA; 1023 BP.
XX
AC ABK10852;
XX
DT 05-JUN-2002 (first entry)
XX
DE cDNA encoding G protein-coupled orphan receptor protein SLT.
XX
KW G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;
KW MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
KW exogenous obesity; hyperinsular obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..1023
FT /*tag= a
FT /product= "SLT"
FT /note= "G protein-coupled orphan receptor"
XX
PN W02020203070-A1.
XX
PD 10-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP005809.
XX
PR 05-JUL-2000; 2000JP-00208254.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX
DR WPI; 2002-164552/21.
XX
P-PSDB; AAU77532.
XX
PT Screening for compounds or salts which alter affinity of melanin-
PT concentrating hormone with its receptor to provide agonists as appetite-
PT stimulating agents and its antagonist for preventing or treating obesity,
PT uses a protein or hormone.
XX
PS Disclosure; Fig 1; 112pp; Japanese.
XX
CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLT. The screened MCH
CC receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocytosis, exogenous obesity and hyperinsular obesity, and also for
CC treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This sequence encodes the G protein-coupled orphan receptor protein, SLT
XX
SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;
Query Match 100.0%; Score 1023; DB 6; Length 1023;
Best Local Similarity 100.0%; Pred. No. 1.8e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAATCCATTTCATGCACTCTTTGGGAACACCTCTGCCGAACCTTTTAAACAAATCTCTGG 60
DB 1 ATGAATCCATTTCATGCACTCTTTGGGAACACCTCTGCCGAACCTTTTAAACAAATCTCTGG 60
QY 61 AATAAAGAGTTTGGCTTATCAAACTCCAGTGTGGTAGATACAGTCATCTCCCTCCATG 120
DB 61 AATAAAGAGTTTGGCTTATCAAACTCCAGTGTGGTAGATACAGTCATCTCCCTCCATG 120
QY 121 ATGGGATTATCTGTTCACAGGCTGTGTGGCAACATCTCTCATCTGTTTACATTAATA 180
DB 121 ATGGGATTATCTGTTCACAGGCTGTGTGGCAACATCTCTCATCTGTTTACATTAATA 180
```

Qy	181	AGATCCAGGAAAAAACAAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTGTG	240
Db	181	AGATCCAGGAAAAAACAAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTGTG	240
Qy	241	GTCCACATAGTTGGAAATGCCCTTTCTTATTCCAAATGGGCCCGAGGGGGAGAGTGGGTG	300
Db	241	GTCCACATAGTTGGAAATGCCCTTTCTTATTCCAAATGGGCCCGAGGGGGAGAGTGGGTG	300
Qy	301	TTTGGGGGCTCTCTGACACCATCATCAATCCCTGGATCTTGTAAACAAATTTGCCCTGT	360
Db	301	TTTGGGGGCTCTCTGACACCATCATCAATCCCTGGATCTTGTAAACAAATTTGCCCTGT	360
Qy	361	AGTGCCATCATGACTGTAAATCAGTGTGGACAGTACTTTGGCCCTCGTCCAAACCAATTCGA	420
Db	361	AGTGCCATCATGACTGTAAATCAGTGTGGACAGTACTTTGGCCCTCGTCCAAACCAATTCGA	420
Qy	421	CTGACAGCTTGGAGAAACAGGTACAAGACATCCGGATCAATTTGGGCTTTGGGCGAGCT	480
Db	421	CTGACAGCTTGGAGAAACAGGTACAAGACATCCGGATCAATTTGGGCTTTGGGCGAGCT	480
Qy	481	TCCTTTATCCGTGGATTCGCCCTGTGGGTCTACTCGAAGGTCAATCAAAATTTAAAGACGGT	540
Db	481	TCCTTTATCCGTGGATTCGCCCTGTGGGTCTACTCGAAGGTCAATCAAAATTTAAAGACGGT	540
Qy	541	GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGACTCTCGGTATACACTTTAT	600
Db	541	GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGACTCTCGGTATACACTTTAT	600
Qy	601	TTGACGATAACAACTTTTTTTTTTCCCTCTACCCCTTGATTTTGGGTGCTATATTTTAATT	660
Db	601	TTGACGATAACAACTTTTTTTTTTCCCTCTACCCCTTGATTTTGGGTGCTATATTTTAATT	660
Qy	661	TTATGCTATACTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCCAGT	720
Db	661	TTATGCTATACTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCCAGT	720
Qy	721	GTACCAAAACAGACAGATGATGAAGTGTACAAAGATGGTGTGGTGTAGTCTTT	780
Db	721	GTACCAAAACAGACAGATGATGAAGTGTACAAAGATGGTGTGGTGTAGTCTTT	780
Qy	781	ATCCTGATGCTGCCCTTATCATGTGATACAACTGTGAACTTACAGATGGAAACAGCC	840
Db	781	ATCCTGATGCTGCCCTTATCATGTGATACAACTGTGAACTTACAGATGGAAACAGCC	840
Qy	841	ACACTGCCCTTCTATGTGGGTATTACTCTCCATCTGTCTCAGCTATGCCAGACAGCAGC	900
Db	841	ACACTGCCCTTCTATGTGGGTATTACTCTCCATCTGTCTCAGCTATGCCAGACAGCAGC	900
Qy	901	ATTAACCTTTTCTCTACCTCTGCTCAGTGGAAATTTCCAGAAACGCTGTGCCTCAAAATC	960
Db	901	ATTAACCTTTTCTCTACCTCTGCTCAGTGGAAATTTCCAGAAACGCTGTGCCTCAAAATC	960
Qy	961	CAAGAAGACGCTGAGAGGAATCAACAAATATGGAAACACTCTGAAATCACTTT	1020
Db	961	CAAGAAGACGCTGAGAGGAATCAACAAATATGGAAACACTCTGAAATCACTTT	1020
Qy	1021	TAG 1023	
Db	1021	TAG 1023	

REFUGEE

RESULT 6  
ABK86285

ABK86285  
ID ABK86285 standard: cDNA: 1023 bp.

XX  
XX

AC ABK8

XX 2017

DT 27-1

XX

DE  
Huma

TGR-associated disorder; signal transduction; retinopathy; hypothyroidism; hypogonadism; retinitis pigmentosa; diabetes insipidus; hyperprolactinaemia; thirst	Location/Qualifiers
sleep disturbance; temperature regulation; blood circadian rhythm.	1..1023
Homo sapiens.	/*tag= a
Key	/product= "Human TGR342 protein"
CDS	

The invention relates to a G-protein coupled receptor polypeptide (GPCR), termed TGR, and its associated nucleic acid. The sequences of the invention are useful for identifying a compound that modulates signal transduction and for identifying a mammal having a TGR-associated disorder. The proteins and nucleic acids are useful in diagnosis and treatment of diseases or conditions such as renal failure, nephritis, hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders, diabetes insipidus, hyperprolactinaemia and disturbances of thirst, sleep, temperature regulation, appetite, blood pressure or any other syndrome or disease associated with the hypothalamus. The sequences can be used in regulation of circadian rhythms, for use as genetic markers for the identification of mutations associated with diseases resulting from GPCR inactivation in particular cell types and for identification of modulators of GPCR signal transduction. This sequence represents cDNA encoding the human TGR342 polypeptide.

Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other; XX

```
Query Match      100.0%; Score 1023; DB 6; Length 1023;
Best Local Similarity 100.0%; Pred. No. 1.8e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0;
```

QY	1	ATGAATCCATTTCATGCATCTTGTGTGGAACACCTCTGCCGAACCTTTTAAACAAATCCTGG	60
Db	1	ATGAATCCATTTCATGCATCTTGTGTGGAACACCTCTGCCGAACCTTTTAAACAAATCCTGG	60
QY	61	AATAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG	120
Db	61	AATAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCATG	120
QY	121	ATTGGGATTATCTGTTCACAGGGCTGGTGGGAACATCCTCATTTGTATTCACTATAATA	180
Db	121	ATTGGGATTATCTGTTCACAGGGCTGGTGGGAACATCCTCATTTGTATTCACTATAATA	180
QY	181	AGATCCAGGAAAAAACAAGTCCCTCGACATCTATATCTGCAACCTGGCTGGGTGATTTC	240



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Db 181 AGATCCAGGAAAAAACAGTCCCTCACATCTATATCTCAACCTGGCTGTGGCTGATTG 240
Qy 241 GTCCACATAGTTGGAATGCTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300
Db 241 GTCCACATAGTTGGAATGCTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300
Qy 301 TTTGGGGGCGCTCTCTGCACCATCATCATCCCTGGATCTTGTGTAACCAATTTGCTGT 360
Db 301 TTTGGGGGCGCTCTCTGCACCATCATCATCCCTGGATCTTGTGTAACCAATTTGCTGT 360
Qy 361 AGTGCCATCATGCTGTAATGAGTGTGACAGGTACTTTGCCCTGCTCAACCAATTTGCA 420
Db 361 AGTGCCATCATGCTGTAATGAGTGTGACAGGTACTTTGCCCTGCTCAACCAATTTGCA 420
Qy 421 CTGACACGTTGGAGAACAGGTACAGACCATCCCGATCAATTTGGGCTTTGGGCGACT 480
Db 421 CTGACACGTTGGAGAACAGGTACAGACCATCCCGATCAATTTGGGCTTTGGGCGACT 480
Qy 481 TCCCTTATCCCTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 TCCCTTATCCCTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 541 GTTGAGAGTTGCTTTTGAATGATGATCCCTGACGATGATCTGCTGATACACTTTAT 600
Db 541 GTTGAGAGTTGCTTTTGAATGATGATCCCTGACGATGATCTGCTGATACACTTTAT 600
Qy 601 TTGACGATTAACAACTTTTTCCTCTACCTTGATTTGGTGTGCTATATTTAATT 660
Db 601 TTGACGATTAACAACTTTTTCCTCTACCTTGATTTGGTGTGCTATATTTAATT 660
Qy 661 TTATGCTACTTGGGAGATGATCAACAGATTAAGGATGCGAGATGCTGCAATCCAGT 720
Db 661 TTATGCTACTTGGGAGATGATCAACAGATTAAGGATGCGAGATGCTGCAATCCAGT 720
Qy 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGGTCTGCTGGTGGTGTAGTCTTT 780
Db 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGGTCTGCTGGTGGTGTAGTCTTT 780
Qy 781 ATCCTGAGTGTGCGCCCTTATCATGTGATACACTGGTGAACCTACAGATGGAACAGCC 840
Db 781 ATCCTGAGTGTGCGCCCTTATCATGTGATACACTGGTGAACCTACAGATGGAACAGCC 840
Qy 841 ACATGCGCTTCTATGTGGTTTATTAACCTCTCACTGTCTGAGTATGCGAGAGAGCAGC 900
Db 841 ACATGCGCTTCTATGTGGTTTATTAACCTCTCACTGTCTGAGTATGCGAGAGAGCAGC 900
Qy 901 ATTAACCTTTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAACGCTGTGCTCAATC 960
Db 901 ATTAACCTTTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAACGCTGTGCTCAATC 960
Qy 961 CAAAGAGAGCGACTGAGAGGAAATCAACATATGGAACACTCTGAAATCACACTTT 1020
Db 961 CAAAGAGAGCGACTGAGAGGAAATCAACATATGGAACACTCTGAAATCACACTTT 1020
Qy 1021 TAG 1023
Db 1021 TAG 1023

```

## RESULT 7

AAD36796

ID AAD36796 standard; cdna; 1023 bp.

XX

AC AAD36796;

XX

DT 24-FEB-2003 (first entry)

DE

XX Human melanin concentrating hormone type 2 receptor (MCH2R) cdna.

XX

KW Melanin concentrating hormone type 2 receptor; MCH2R; hyperphagic;

XX

KW hyperphagic; body weight; locomotor activity; stress; anxiety;

XX

KW sleep disorder; fatigue; circadian rhythm; energy metabolism; pain;

KW cancer; sexual dysfunction; diabetes; human; ss.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1023

FT /\*tag= a

FT /product= "MCH2R"

XX /note= "Melanin concentrating hormone type 2 receptor"

PN W0200277168-A2.

XX 03-OCT-2002.

XX 19-MAR-2002; 2002WO-US008413.

XX 22-MAR-2001; 2001US-0278061P.

PA (MERI ) MERCK &amp; CO INC.

XX Qian S, Marsh DJ;

XX WPI; 2003-018901/01.

XX P-PSDB; AAE14795.

DR MCH1R deficient mouse with an alteration in one or both alleles, useful for screening of compounds as a research tool and for achieving useful effects for locomotor activity, stress, anxiety, fatigue, circadian rhythm or sleep.

PS Disclosure; Page 31; 35pp; English.

XX The invention relates to a melanin concentrating hormone type 1 receptor (MCH1R) deficient mouse whose genome comprises an alteration in one or both MCH1R alleles, where the alteration substantially reduces expression of a functional MCH1R. The invention also relates to a method of measuring the effect of a compound on a MCH1R deficient mouse and measuring one or more phenotypes associated with MCH1R activity e.g. hyperphagic or hypophagic activity, body weight, locomotor activity, stress, anxiety, sleep, fatigue, circadian rhythm and energy metabolism. The methods and composition of the present invention are useful for screening of compounds that are further used as a research tool and for treating weight loss or weight gain, reducing pain, stress, anxiety, and treating cancer, sexual dysfunction, diabetes, locomotor deficits, fatigue or sleep disorders. The present sequence is human melanin concentrating hormone type 2 receptor (MCH2R) cdna used in a method of the invention

XX Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 7; Length 1023;

Best Local Similarity 100.0%; Pred. No. 1.8e-295;

Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATCCATTTCATGCATCTTTGTGGACACCTCTGCCGAACCTTTTAAACAATCTGG 60

Db 1 ATGAATCCATTTCATGCATCTTTGTGGACACCTCTGCCGAACCTTTTAAACAATCTGG 60

Qy 61 AATAAGAGTTTGCCTTATCAAACTGCCAGTGTGTAGATACAGTCATCCCTCCCTCCATG 120

Db 61 AATAAGAGTTTGCCTTATCAAACTGCCAGTGTGTAGATACAGTCATCCCTCCCTCCATG 120

Qy 121 ATTGGGATTAATCTGTTCACAGGGCTGGTTGGCAACATCTCTATTGTATTCACTATAA 180

Db 121 ATTGGGATTAATCTGTTCACAGGGCTGGTTGGCAACATCTCTATTGTATTCACTATAA 180

Qy 181 AGATCCAGGAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTG 240

Db 181 AGATCCAGGAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTG 240

Qy 241 GTCCACATAGTTGGAATGCTTTCTTTTATTCACCAATGGCCCGAGGGAGAGTGGGTG 300

Db 241 GTCCACATAGTTGGAATGCTTTCTTTTATTCACCAATGGCCCGAGGGAGAGTGGGTG 300

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QY 301 TTGGGGGGCTCTGCGACCATCATCATCCCTGGATACATGTAACCAATTTGCCGTG 360
Db 301 TTGGGGGGCTCTGCGACCATCATCATCCCTGGATACATGTAACCAATTTGCCGTG 360
QY 361 AGTGCATCATGACTGTAATGAGTGGACAGTACTTTGCCCTGCTCAACCAATTTGCA 420
Db 361 AGTGCATCATGACTGTAATGAGTGGACAGTACTTTGCCCTGCTCAACCAATTTGCA 420
QY 421 CTGACAGTTGGAGAACAGGTACAGACCATCCGGATCAATTTGGGCTTTGGGAGCT 480
Db 421 CTGACAGTTGGAGAACAGGTACAGACCATCCGGATCAATTTGGGCTTTGGGAGCT 480
QY 481 TCCTTTATCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 TCCTTTATCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GTTGAGAGTTGCTTTTGGATTTGACATCCCTGAGATGCTGCTGCTGCTGCTGCTGCT 600
Db 541 GTTGAGAGTTGCTTTTGGATTTGACATCCCTGAGATGCTGCTGCTGCTGCTGCTGCT 600
QY 601 TTGACGATCAACATTTTTCCTCTACCCCTGATTTTGGTGGCTGCTGCTGCTGCTGCTGCT 660
Db 601 TTGACGATCAACATTTTTCCTCTACCCCTGATTTTGGTGGCTGCTGCTGCTGCTGCTGCT 660
QY 661 TTATGCTATCTTGGAGATGATCAACAGATTAAGGATCCAGATGCTGCTGCTGCTGCTGCT 720
Db 661 TTATGCTATCTTGGAGATGATCAACAGATTAAGGATCCAGATGCTGCTGCTGCTGCTGCT 720
QY 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 ATCTGAGTGCCTCCCTTATCATGTGATACAACTGGTGAATACAGATGGAACAGCC 840
Db 781 ATCTGAGTGCCTCCCTTATCATGTGATACAACTGGTGAATACAGATGGAACAGCC 840
QY 841 ACACCTGGCTTCTATGCTGCTTATACCTCTCCATCTGCTCAGTATGCCAGCAGCAGC 900
Db 841 ACACCTGGCTTCTATGCTGCTTATACCTCTCCATCTGCTCAGTATGCCAGCAGCAGC 900
QY 901 ATTAACCTTTCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 ATTAACCTTTCTTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 CAAAGAGAGCGACTCAGAGAGAAATCAACATATGGGAAACACTCTGAAATCAACACTTT 1020
Db 961 CAAAGAGAGCGACTCAGAGAGAAATCAACATATGGGAAACACTCTGAAATCAACACTTT 1020
QY 1021 TAG 1023
Db 1021 TAG 1023

```

## RESULT 8

AD54241  
ID AAD54241 standard; cDNA; 1023 BP.

XX AC  
XX AC  
XX AC

DT 17-JUN-2003 (first entry)

XX Human melanin-concentrating hormone-2 receptor (MCH-2R) cDNA.

XX Melanin-concentrating hormone-2 receptor; MCH-2R; appetite; MCH-1R;  
KW melanin-concentrating hormone; MCH; receptor; human; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH 1..1023  
FT /\*tag= a  
FT /product= "Human MCH-2R protein"

XX WO200297037-A2.  
XX 05-DEC-2002.  
XX 28-MAY-2002; 2002WO-US016513.  
XX 31-MAY-2001; 2001US-0294806P.  
XX (MERI) MERCK & CO INC.  
XX Bednarek M;  
XX WPI; 2003-201270/19.  
XX P-PSDB; AAE35562.  
XX Novel truncated melanin-concentrating hormone analog peptide active at  
PT melanin-concentrating hormone-2 receptor, or its labeled derivative or  
PT salt, useful for increasing weight or appetite in a subject.  
XX Example 1; Page 59; 30pp; English.  
XX The invention relates to truncated melanin-concentrating hormone (MCH)  
CC analogue peptide active at melanin-concentrating hormone-2 receptor (MCH-  
CC 2R), or its labelled derivative or salt, useful for increasing weight or  
CC appetite in a subject. The peptide is useful for screening for a compound  
CC able to bind MCH-2R. It is useful for increasing weight or appetite in a  
CC subject having an MCH-2R. It is useful for measuring the ability of a  
CC compound to decrease weight or appetite in a subject having MCH-2R. It is  
CC useful to screen for MCH agonists, to explore differences between MCH-1R  
CC and MCH-2R and to distinguish between the presence of MCH-1R and MCH-2R.  
XX The present sequence is human MCH-2R cDNA

Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 7; Length 1023;

Best Local Similarity 100.0%; Pred. No. 1.8e-295;

Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATCCATTTTCATGATCTTGTGGACACACTCTGCGGAACTTTTAAACAAATCCTGG 60  
Db 1 ATGAATCCATTTTCATGATCTTGTGGACACACTCTGCGGAACTTTTAAACAAATCCTGG 60  
QY 61 AATAAAGAGTTTGTATCAAACTGCCAGTGTGGTAGATACATCTCCCTCCATG 120  
Db 61 AATAAAGAGTTTGTATCAAACTGCCAGTGTGGTAGATACATCTCCCTCCATG 120  
QY 121 ATTGGGATTTATCTTCAACAGGCTGGTTGGCAACATCTCTATTCTTCACTATAATA 180  
Db 121 ATTGGGATTTATCTTCAACAGGCTGGTTGGCAACATCTCTATTCTTCACTATAATA 180  
QY 181 AGATCCAGGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGCTGCTGCTGCTGCTG 240  
Db 181 AGATCCAGGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGCTGCTGCTGCTGCTG 240  
QY 241 GTCCACATAGTTGGATGCTTTTCTATTTCACCAATGGCCCGAGGGGAGAGTGGTG 300  
Db 241 GTCCACATAGTTGGATGCTTTTCTATTTCACCAATGGCCCGAGGGGAGAGTGGTG 300  
QY 301 TTTGGGGGCTCTCTGACCATCATCACATCCCTGGATCTTTGTAACCAATTTGCTGT 360  
Db 301 TTTGGGGGCTCTCTGACCATCATCACATCCCTGGATCTTTGTAACCAATTTGCTGT 360  
QY 361 AGTGCCATCATGATGTAATGAGTGTGGACAGTACTTTGCCCTGCTCAACCAATTTGCA 420  
Db 361 AGTGCCATCATGATGTAATGAGTGTGGACAGTACTTTGCCCTGCTCAACCAATTTGCA 420  
QY 421 CTGACAGTTGGAGAACAGGTACAGACCATCCGGATCAATTTGGGCTTTGGGAGCT 480  
Db 421 CTGACAGTTGGAGAACAGGTACAGACCATCCGGATCAATTTGGGCTTTGGGAGCT 480  
QY 481 TCCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Db 481 TCCTTTATCCCTGGCANTGCTCTGCGGTCTACTCGAAGGTCATCAAAATTTAAAGACGGT 540  
QY 541 GTTGAGAGTTGGCTTTTGAATTTGACATCCCTGACGATGACTCTGGTATACACTTTAT 600  
Db 541 GTTGAGAGTTGGCTTTTGAATTTGACATCCCTGACGATGACTCTGGTATACACTTTAT 600  
QY 601 TTGAGAGTAACAACTTTTTCCTTCCCTCTACCCCTGATGATTTGGTGTCTATTTAAAT 660  
Db 601 TTGAGAGTAACAACTTTTTCCTTCCCTCTACCCCTGATGATTTGGTGTCTATTTAAAT 660  
QY 661 TTATGCTATCTTGGAGATGATCAACAGATAAGGATGCCAGATGCTGCAATCCCAAT 720  
Db 661 TTATGCTATCTTGGAGATGATCAACAGATAAGGATGCCAGATGCTGCAATCCCAAT 720  
QY 721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGTCTGCTGGTGTCTGTTT 780  
Db 721 GTACCAAAACAGAGAGTGATGAAGTTGACAAAGATGGTGTCTGCTGGTGTCTGTTT 780  
QY 781 ATCTGAGTGTGCCCCCTTATCATGTGATACAACTGGTGAACCTTACAGATGGAACAGGCC 840  
Db 781 ATCTGAGTGTGCCCCCTTATCATGTGATACAACTGGTGAACCTTACAGATGGAACAGGCC 840  
QY 841 ACATGCGCCTTCTATGTGGTGTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGC 900  
Db 841 ACATGCGCCTTCTATGTGGTGTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGC 900  
QY 901 ATTAACCCCTTTCTCTACATCTGCTGAGTGAAGTTTCCAGAACTGCTGCTCAATC 960  
Db 901 ATTAACCCCTTTCTCTACATCTGCTGAGTGAAGTTTCCAGAACTGCTGCTCAATC 960  
QY 961 CAAAGAGAGCGACTGAGAGGAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020  
Db 961 CAAAGAGAGCGACTGAGAGGAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020  
QY 1021 TAG 1023  
Db 1021 TAG 1023

RESULT 9  
AAL57671  
ID AAL57671 standard; cDNA; 1023 BP.  
AC AAL57671;  
XX  
DT 16-OCT-2003 (first entry)  
DE Human melanin-concentrating hormone type 2 receptor (MCH-2R) cDNA.  
XX  
KW Human; melanin-concentrating hormone; hMCH; MCH type 1 receptor; MCH-1R;  
KW MCH-1R agonist; anti-HIV; anabolic; immunomodulator; increasing weight;  
KW increasing appetite; weight loss disorder; anorexia; AIDS; wasting;  
KW cachexia; frail elderly disease; food intake;  
KW hypothalamus neuronal cell body; lateral hypothalamus perikaryon;  
KW zona inerta; orexigenic; MCH type 2 receptor; MCH-2R; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1023  
FT /\*tag= a  
FT /product= "Human MCH-2R protein"  
XX  
XX WO2003060091-A2.  
XX  
XX 24-JUL-2003.  
XX  
XX 06-JAN-2003; 2003WO-US000241.  
XX  
XX 09-JAN-2002; 2002US-0347191P.  
XX  
XX (NERI ) MERCK & CO INC.

PI Bednarek MA;  
XX WPI; 2003-646040/61.  
DR P-PSDB; AAO27467.  
XX  
PT New optionally substituted truncated human melanin-concentrating hormone  
PT (hMCH) peptides are hMCH-1 agonists, useful for increasing  
PT appetite/weight.  
XX  
PS Example 1; Page 20-21; 55pp; English.  
XX  
CC This invention relates to novel truncated human melanin-concentrating  
CC hormone (hMCH) analogue peptides selectively active on the MCH type 1  
CC receptor (MCH-1R). MCH has been localized to the neuronal cell bodies of  
CC the hypothalamus which are implicated in the control of food intake,  
CC including perikarya of the lateral hypothalamus and zona inerta. The  
CC primary mode of action of MCH is to promote feeding (orexigenic). The  
CC peptides of the invention, MCH-1R agonists, may have anti-HIV, anabolic  
CC or immunomodulator activities. The peptides may be useful for increasing  
CC weight/appetite in a subject having an MCH-1R. They may also be useful  
CC for measuring the ability of a compound to decrease weight/appetite in a  
CC subject having an MCH-1R which involves administering the peptides to the  
CC subject to produce weight/appetite increase, administering the compound,  
CC and measuring the change in weight or appetite of the subject. The  
CC peptides may therefore be useful for treating disorders accompanied by  
CC weight loss including anorexia, AIDS, wasting, cachexia and frail elderly  
CC diseases. The invention offers the advantages of ease of synthesis and/or  
CC increased solubility in physiological buffers. The present sequence is  
CC the cDNA sequence encoding the human melanin-concentrating hormone (hMCH)  
CC type 2 receptor (MCH-2R) against which the peptides of the invention are  
CC specifically not targeted.  
XX  
SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 8; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 1.8e-295;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATCCATTTTCATGATCTTTTGGAAACACCTCTGCCGAACCTTTTAAACAAATCTGG 60  
Db 1 ATGAATCCATTTTCATGATCTTTTGGAAACACCTCTGCCGAACCTTTTAAACAAATCTGG 60  
QY 61 AATAAGAGTTGGTCTTATCAAACTGCCAGTGTGTAGATACAGTCATCTCCCTCCATG 120  
Db 61 AATAAGAGTTGGTCTTATCAAACTGCCAGTGTGTAGATACAGTCATCTCCCTCCATG 120  
QY 121 ATTGGGATTTCTCTTCAACAGGGCTGTGTGGCAACATCTCTCATTTGATTCATATAATA 180  
Db 121 ATTGGGATTTCTCTTCAACAGGGCTGTGTGGCAACATCTCTCATTTGATTCATATAATA 180  
QY 181 AGATCCAGGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTG 240  
Db 181 AGATCCAGGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTG 240  
QY 241 GTCCACATAGTTGGAATGCCCTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300  
Db 241 GTCCACATAGTTGGAATGCCCTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTG 300  
QY 301 TTTGGGGGGCTCTCTGCAACCATCATCATCTCCCTGGATCTTTGTAACCAATTTGCCGT 360  
Db 301 TTTGGGGGGCTCTCTGCAACCATCATCATCTCCCTGGATCTTTGTAACCAATTTGCCGT 360  
QY 361 AGTGCCATCATGACTGTAAATGAGTGTGACAGGTTACTTTGCCCTCGCTCCACCAATTCGA 420  
Db 361 AGTGCCATCATGACTGTAAATGAGTGTGACAGGTTACTTTGCCCTCGCTCCACCAATTCGA 420  
QY 421 CTGACACCTTGGAGAACAAAGGTACAAGACCATCCCGATCAATTTGGGGCTTTGGGGCAGCT 480  
Db 421 CTGACACCTTGGAGAACAAAGGTACAAGACCATCCCGATCAATTTGGGGCTTTGGGGCAGCT 480  
QY 481 TCCTTTATCTCGGCAATTCCTGCTGTGGGTCTACTCGAAGGTGTCATCAATTTAAAGACGGT 540  
Db 481 TCCTTTATCTCGGCAATTCCTGCTGTGGGTCTACTCGAAGGTGTCATCAATTTAAAGACGGT 540

QY 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGACTCTGGTATACACTTTAT 600  
 DB 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGACTCTGGTATACACTTTAT 600  
 QY 601 TTGACGATACAACTTTTTCCTCTACCTTGAATTTGGTGTGCTATATTTAAT 660  
 DB 601 TTGACGATACAACTTTTTCCTCTACCTTGAATTTGGTGTGCTATATTTAAT 660  
 QY 661 TTATGCTATCTGGGAGATGTATCAACAGATAAGATGCCAGATGCTGCATCCAGT 720  
 DB 661 TTATGCTATCTGGGAGATGTATCAACAGATAAGATGCCAGATGCTGCATCCAGT 720  
 QY 721 GTACCAAAACAGAGATGATGAAGTGAACAAAGATGGTGTGCTGGTGTGCTTT 780  
 DB 721 GTACCAAAACAGAGATGATGAAGTGAACAAAGATGGTGTGCTGGTGTGCTTT 780  
 QY 781 ATCTGAGTCTGCCCTTATCATGTGATACAACTGGTGAACCTTACAGATGGAACAGCCC 840  
 DB 781 ATCTGAGTCTGCCCTTATCATGTGATACAACTGGTGAACCTTACAGATGGAACAGCCC 840  
 QY 841 ACATGCTCTTATGTTGGTTATTAACCTTCCATCTGCTCAGTATCCAGCAGCAGC 900  
 DB 841 ACATGCTCTTATGTTGGTTATTAACCTTCCATCTGCTCAGTATCCAGCAGCAGC 900  
 QY 901 ATTAACCCCTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAAGCTGCTGCAAAATC 960  
 DB 901 ATTAACCCCTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAAGCTGCTGCAAAATC 960  
 QY 961 CAAAGAGAGCGACTGAGAGGAGAAATCAACAATATGAGAAACACTCTGAAATCACAATTT 1020  
 DB 961 CAAAGAGAGCGACTGAGAGGAGAAATCAACAATATGAGAAACACTCTGAAATCACAATTT 1020  
 QY 1021 TAG 1023  
 DB 1021 TAG 1023

RESULT 10  
 AAD61085  
 ID AAD61085 standard; cdna; 1023 BP.  
 AC AAD61085;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human G protein-coupled receptor (GPCR), HGPBMY9 cdna.  
 KW Human; G protein-coupled receptor; GPCR; HGPBMY9; therapy; brain; lung;  
 KW colon; testes; gastrointestinal; reproductive system; asthma; diabetes;  
 KW noctropic; gynaecological; Alzheimer's disease; neuroprotective; cancer;  
 KW receptor; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1023  
 FT /\*tag= a  
 FT /product= "Human G protein-coupled receptor, HGPBMY9"  
 XX  
 XX US2003096300-A1.  
 XX  
 XX 22-MAY-2003.  
 XX  
 XX 26-SEP-2001; 2001US-00964923.  
 XX  
 XX 27-SEP-2000; 2000US-0235709P.  
 XX  
 XX 16-JAN-2001; 2001US-0261775P.  
 XX  
 XX 02-AUG-2001; 2001US-0309625P.  
 XX  
 XX (FEDE/) FEDER J N.  
 XX (MINT/) MINTIER G.  
 XX (RAMA/) RAMANATHAN C S.

(HAWK/) HAWKEN D R.  
 (CACA/) CACACE A.  
 Feder JN, Mintier G, Ramanathan CS, Hawken DR, Cacace A;  
 WPI; 2003-786987/74.  
 P-PSDB; ABW00463.  
 New human G-protein coupled receptor and its encoding polynucleotide  
 useful for treating and diagnosing conditions such as neurological  
 disorders and disorders of the testes.  
 Claim 1; Fig 1; Opp; English.  
 The invention relates to human G protein-coupled receptor (GPCR),  
 HGPBMY9 and its nucleic acid sequence. The invention is useful for  
 preventing, treating, or ameliorating a medical condition related to the  
 brain, lung, colon, testes, neural, gastrointestinal, pulmonary, or  
 reproductive system. Detecting mutations in HGPBMY9 DNA or determining  
 the level of expression of HGPBMY9 is useful in diagnosing disease.  
 HGPBMY9 nucleic acid, polypeptide and agents that control the level of  
 expression or activity of HGPBMY9 may be useful in treating conditions  
 such as cancer, Alzheimer's disease, asthma, and diabetes. The present  
 sequence is human HGPBMY9 cdna  
 XX  
 SQ Sequence 1023 BP; 265 A; 230 C; 221 G; 307 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1023; DB 9; Length 1023;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-295;  
 Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAATCCATTTCATGTCATCTTGTGGAACACCTCTGCCGAACCTTTTAAACAATCTCTG 60  
 DB 1 ATGAATCCATTTCATGTCATCTTGTGGAACACCTCTGCCGAACCTTTTAAACAATCTCTG 60  
 QY 61 AATAAGAGTTTGTCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCTCCCTTCATG 120  
 DB 61 AATAAGAGTTTGTCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCTCCCTTCATG 120  
 QY 121 ATTGGGATATCTGTTCAACAGGCTGGTTGGCAACATCTCTATTCTGTTTCACTATAATA 180  
 DB 121 ATTGGGATATCTGTTCAACAGGCTGGTTGGCAACATCTCTATTCTGTTTCACTATAATA 180  
 QY 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGTGTGGTGTATTG 240  
 DB 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGTGTGGTGTATTG 240  
 QY 241 GTCCACATAGTTGGAATGCCCTTTTCTTATTACCAATGGSCCGAGGGGAGAGTGGTG 300  
 DB 241 GTCCACATAGTTGGAATGCCCTTTTCTTATTACCAATGGSCCGAGGGGAGAGTGGTG 300  
 QY 301 TTTGGGGGGCTCTCTGCACCATCATCACATCCCTGGATACTTGTAAACCAATTTGCTGT 360  
 DB 301 TTTGGGGGGCTCTCTGCACCATCATCACATCCCTGGATACTTGTAAACCAATTTGCTGT 360  
 QY 361 AGTCCCATCATGACTGTAATGAGTGTGGAAGTATCTTTGCCCTCTGTCACCACTTCGA 420  
 DB 361 AGTCCCATCATGACTGTAATGAGTGTGGAAGTATCTTTGCCCTCTGTCACCACTTCGA 420  
 QY 421 CTGACAGTTTGGAGAACAGGTACAGACCATCCGGATCAATTTGGGCCCTTTGGGAGCT 480  
 DB 421 CTGACAGTTTGGAGAACAGGTACAGACCATCCGGATCAATTTGGGCCCTTTGGGAGCT 480  
 QY 481 TCCTTTATCTGGCATTCCTGTCTGGTGTCTACGAAGGTATCAAAATTAAGACGGT 540  
 DB 481 TCCTTTATCTGGCATTCCTGTCTGGTGTCTACGAAGGTATCAAAATTAAGACGGT 540  
 QY 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGACTCTGGTATACACTTTAT 600  
 DB 541 GTTGAGAGTTGTGCTTTTGATTTGACATCCCTGACGATGACTCTGGTATACACTTTAT 600  
 QY 601 TTGACGATACAACTTTTTCCTCTACCTTGAATTTGGTGTGCTATATTTAAT 660

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Db 601 TTGACGATAACAACCTTTTTCCTCTACCTTGATTTTGGTGTGCTATATTTTAATT 660
QY 661 TTATGCTATACCTTGGAGATGATCAACAGATAAGGATGCCAGATGCTGCAATCCCACT 720
Db 661 TTATGCTATACCTTGGAGATGATCAACAGATAAGGATGCCAGATGCTGCAATCCCACT 720
QY 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGGTCTGCTGGTGTGTAGTCTTT 780
Db 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGGTCTGCTGGTGTGTAGTCTTT 780
QY 781 ATCTCAGTGTGCTCCCTTATCATGTGATACAACTGGTGAATTTACAGATGAAACAGGCC 840
Db 781 ATCTCAGTGTGCTCCCTTATCATGTGATACAACTGGTGAATTTACAGATGAAACAGGCC 840
QY 841 ACACCTGGCTTATATGCGGTATATACCTCTCACTGTCTCAGCTATGCCAGCAGC 900
Db 841 ACACCTGGCTTATATGCGGTATATACCTCTCACTGTCTCAGCTATGCCAGCAGC 900
QY 901 ATTACCCCTTTCTCTACATCTCTGCTGAGTGAATTTCCAGAAACGCTGCTCAAAATC 960
Db 901 ATTACCCCTTTCTCTACATCTCTGCTGAGTGAATTTCCAGAAACGCTGCTCAAAATC 960
QY 961 CAAAGAGAGCGACTGAGAGGAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
Db 961 CAAAGAGAGCGACTGAGAGGAATCAACAATATGGGAAACACTCTGAAATCACACTTT 1020
QY 1021 TAG 1023
Db 1021 TAG 1023

RESULT 11
ID ABK10848 standard; DNA; 1035 BP.
AC ABK10848;
XX
DT 05-JUN-2002 (first entry)
XX
DE DNA encoding G protein-coupled orphan receptor protein SLT.
XX
KW G protein-coupled orphan; receptor; SLT; melanin-concentrating hormone;
KW MCH; appetite-stimulating agent; obesity; malignant mastocytosis;
KW exogenous obesity; hyperinsular obesity; sexual function disorder;
KW overpowering intermittent pain; still born; uterus rupture;
KW premature birth; Prader-Willi syndrome; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..1029
FT FT /*tag= a
FT FT /product= "SLT"
FT FT /note= "G protein-coupled orphan receptor"
XX
PN WO200203070-A1.
XX
PD 10-JAN-2002.
XX
PF 04-JUL-2001; 2001WO-JP005809.
XX
PR 05-JUL-2000; 2000JP-00208254.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Mori M, Shimomura Y, Harada M, Sugo T, Shintani Y;
XX
DR WPI; 2002-164552/21.
DR P-PSDB; AAU77532.
XX
PT Screening for compounds or salts which alter affinity of melanin-
PT concentrating hormone with its receptor to provide agonists as appetite-
PT stimulating agents and its antagonist for preventing or treating obesity,

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PT uses a protein or hormone.
XX
PS Example 2; Page 96-97; 112pp; Japanese.
XX
CC The invention describes a method of screening for compounds or their
CC salts that can change affinity of melanin-concentrating hormone (MCH)
CC with its G protein-coupled orphan receptor protein, SLT. The screened MCH
CC receptor agonists are useful as appetite-stimulating agents and its
CC antagonist for preventing or treating obesity e.g. malignant
CC mastocytosis, exogenous obesity and hyperinsular obesity, and also for
CC treating sexual function disorders, overpowering intermittent pains,
CC still borns, uterus rupture, premature birth and Prader-Willi syndrome.
CC This sequence encodes the G protein-coupled orphan receptor protein, SLT
XX
SQ Sequence 1035 BP; 268 A; 233 C; 224 G; 310 T; 0 U; 0 Other;

Query Match 100.0%; Score 1023; DB 6; Length 1035;
Best Local Similarity 100.0%; Pred. No. 1.9e-295;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATCATTTTCAATGATCTTGTGGAACACCTCTGCCGAACCTTTTAAACAAATCCCTGG 60
Db 7 ATGAATCATTTTCAATGATCTTGTGGAACACCTCTGCCGAACCTTTTAAACAAATCCCTGG 66
QY 61 AATAAGAGTTTGTCTTATCAAACTGCCAGTGTGTAGATACAGTCATCCTCCCTTCCATG 120
Db 67 AATAAGAGTTTGTCTTATCAAACTGCCAGTGTGTAGATACAGTCATCCTCCCTTCCATG 126
QY 121 ATTGGGATTTATCTTTCAACAGGGCTGGTTGGCAACATCTCTATTGTATTACATATAATA 180
Db 127 ATTGGGATTTATCTTTCAACAGGGCTGGTTGGCAACATCTCTATTGTATTACATATAATA 186
QY 181 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTG 240
Db 187 AGATCCAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTG 246
QY 241 GTCCACATAGTTGGAATGCCCTTTTCTTATTACCAATGGGCCCGAGGGGAGAGTGGGTG 300
Db 247 GTCCACATAGTTGGAATGCCCTTTTCTTATTACCAATGGGCCCGAGGGGAGAGTGGGTG 306
QY 301 TTTGGGGGGCTCTCTGCAACCATCATCATCTCCCTGATCTTGTAAACCAATTTTGCCTGT 360
Db 307 TTTGGGGGGCTCTCTGCAACCATCATCATCTCCCTGATCTTGTAAACCAATTTTGCCTGT 366
QY 361 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCCTGCTCCAAACATTTCGA 420
Db 367 AGTGCCATCATGACTGTAATGAGTGTGGACAGGTACTTTGCCCCTGCTCCAAACATTTCGA 426
QY 421 CTGACAGCTTGGAGAAACAAGGTACAAGCATCCCGATCAATTTGGGCCCTTTGGGCAAGCT 480
Db 427 CTGACAGCTTGGAGAAACAAGGTACAAGCATCCCGATCAATTTGGGCCCTTTGGGCAAGCT 486
QY 481 TCCTTTATCTCTGGCATTTGCCCTTGTCTGCTGCTACTCGAAGGTCAATTAATTTAAAGACGGT 540
Db 487 TCCTTTATCTCTGGCATTTGCCCTTGTCTGCTGCTACTCGAAGGTCAATTAATTTAAAGACGGT 546
QY 541 GTTGAGAGTTGTGCTTTTGTATTTGACATCCCTGACAGATGCTCTGCTATACACTTTAT 600
Db 547 GTTGAGAGTTGTGCTTTTGTATTTGACATCCCTGACAGATGCTCTGCTATACACTTTAT 606
QY 601 TTGACGATAACAACCTTTTTCCTCTACCTTGTATTTTGGTGTGCTATATTTTAATT 660
Db 607 TTGACGATAACAACCTTTTTCCTCTACCTTGTATTTTGGTGTGCTATATTTTAATT 666
QY 661 TTATGCTATACCTTGGAGATGATCAACAGATAAGGATGCCAGATGCTGCAATCCCACT 720
Db 667 TTATGCTATACCTTGGAGATGATCAACAGATAAGGATGCCAGATGCTGCAATCCCACT 726
QY 721 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGGTCTGCTGGTGTGTAGTCTTT 780
Db 727 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGGTCTGCTGGTGTGTAGTCTTT 786
QY 781 ATCTCAGTGTGCTCCCTTATCATGTGATACAACTGGTGAATTTACAGATGAAACAGGCC 840

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Db 787 ATCTGAGTCTGCCCTTATCATGTGATACAACTGGTGAATTCAGATGGAACAGCCC 846  
QY 841 ACACCTGCTTCTATGCTGTTATACCTCTCCATCTGTCTAGTATGCCAGCAGC 900  
Db 847 ACACCTGCTTCTATGCTGTTATACCTCTCCATCTGTCTAGTATGCCAGCAGC 906  
QY 901 ATTAACCTTTCTCATCTCTGCTGAGTGGAAATTCAGAAAGCTGTGCCTCAATC 960  
Db 907 ATTAACCTTTCTCATCTCTGCTGAGTGGAAATTCAGAAAGCTGTGCCTCAATC 966  
QY 961 CAAGAGAGCGACTGAGAGGAAATCAACAATATGGAACACTCTGAAATCACACTTT 1020  
Db 967 CAAGAGAGCGACTGAGAGGAAATCAACAATATGGAACACTCTGAAATCACACTTT 1026  
QY 1021 TAG 1023  
Db 1027 TAG 1029

RESULT 12  
AAS42862  
ID AAS42862 standard; cDNA; 1965 BP.  
XX AC AAS42862;  
XX 18-DEC-2001 (first entry)  
XX Human G Protein-Coupled Receptor (GPCR) cDNA #57.  
XX Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;  
XX attention deficit disorder; anxiety; depression; bipolar disorder; ss;  
XX neurological disorder; Huntington's disease; dementia; obesity; anorexia;  
XX metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;  
XX type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;  
XX cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;  
XX viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;  
XX antidepressant; anorectic; PCR primer; gene therapy.  
OS Homo sapiens.  
XX W0200162797-A2.  
XX 30-AUG-2001.  
XX 23-FEB-2001; 2001WO-US005676.  
XX 23-FEB-2000; 2000US-0184247P.  
XX 23-FEB-2000; 2000US-0184303P.  
XX 23-FEB-2000; 2000US-0184304P.  
XX 23-FEB-2000; 2000US-0184305P.  
XX 23-FEB-2000; 2000US-0184397P.  
XX 02-MAR-2000; 2000US-0186457P.  
XX 03-MAR-2000; 2000US-0186810P.  
XX 09-MAR-2000; 2000US-0188064P.  
XX 13-MAR-2000; 2000US-0188880P.  
XX 03-APR-2000; 2000US-0194344P.  
XX 23-JUN-2000; 2000US-0213861P.  
XX 11-JUL-2000; 2000US-0217369P.  
XX 14-JUL-2000; 2000US-0217370P.  
XX 20-JUL-2000; 2000US-0218337P.  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
XX Vogeli G, Wood LS, Parodi LA, Lind P;  
XX WPI; 2001-570628/64.  
XX P-PSDB; AAU25610.

New isolated nucleic acid encoding a new G-protein coupled receptor  
PT polypeptide for detecting receptor modulators that can treat mental  
PT disorders, such as schizophrenia, anxiety, depression, or obesity.

XX Claim 4; Page 92-93; 279pp; English.  
XX Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for  
CC cDNA molecules encoding human G-protein coupled receptor (GPCR)  
CC polypeptides. The protein and DNA sequences of the invention can be used  
CC to identify compounds which bind to GPCR polypeptides and in screening  
CC for compounds that modulate GPCR activity. By screening a human subject  
CC for the presence of mutations in GPCR DNA, a GPCR-related disorder or a  
CC genetic predisposition can be diagnosed. The sequences can also be used  
CC for treatment and prevention of mental disorders such as schizophrenia,  
CC attention deficit disorder, anxiety, depression, dementia and bipolar  
CC disorder, neurological disorders such as Huntington's disease,  
CC Parkinson's disease and Tourette's syndrome, metabolic disorders such as  
CC obesity, anorexia and type 2 diabetes, cardiovascular disorders such as  
CC thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,  
CC viral infections caused by HIV and cancers  
XX Sequence 1965 BP; 547 A; 422 C; 402 G; 594 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1023; DB 4; Length 1965;  
Best Local Similarity 100.0%; Pred. No. 2.5e-295;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATCCATTTTCATGCAATCTTGTGGAACACCTCTCGGAACCTTTTAAACAAATCTCGG 60  
Db 58 ATGAATCCATTTTCATGCAATCTTGTGGAACACCTCTCGGAACCTTTTAAACAAATCTCGG 117  
QY 61 AATAAAGAGTTTGGTTATCAAACTGCCAGTGTGTAGATACAGTCATCTCCCTCCATG 120  
Db 118 AATAAAGAGTTTGGTTATCAAACTGCCAGTGTGTAGATACAGTCATCTCCCTCCATG 177  
QY 121 ATTGGGATTAATCTCTCAACAGGCTGTGTGGCAACATCTCTCATTTTCACTATAATA 180  
Db 178 ATTGGGATTAATCTCTCAACAGGCTGTGTGGCAACATCTCTCATTTTCACTATAATA 237  
QY 181 AGATCCAGGAAAAAAGCAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTG 240  
Db 238 AGATCCAGGAAAAAAGCAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTG 297  
QY 241 GTCCACATAGTTGGAATGCCCTTTCTTATTACCAATGGGCGGAGGAGAGTGGTG 300  
Db 298 GTCCACATAGTTGGAATGCCCTTTCTTATTACCAATGGGCGGAGGAGAGTGGTG 357  
QY 301 TTTGGGGGGCTCTCTGCACCATCATCATCCCTGGATATTTTAAACCAATTTGCCCTGT 360  
Db 358 TTTGGGGGGCTCTCTGCACCATCATCATCCCTGGATATTTTAAACCAATTTGCCCTGT 417  
QY 361 AGTGCATCATGATGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCCAACCAATTCGA 420  
Db 418 AGTGCATCATGATGTAATGAGTGTGGACAGGTACTTTGCCCTCGTCCCAACCAATTCGA 477  
QY 421 CTGACACGTTGGAGAACAAAGGTACAAGACCATCCGGATCAATTTGGGCGCTTTGGGACGT 480  
Db 478 CTGACACGTTGGAGAACAAAGGTACAAGACCATCCGGATCAATTTGGGCGCTTTGGGACGT 537  
QY 481 TCCCTTTATCTGGCATTGCCCTGTCTGGGTCTATCTCGAAGGTCAATTAATAAGACGT 540  
Db 538 TCCCTTTATCTGGCATTGCCCTGTCTGGGTCTATCTCGAAGGTCAATTAATAAGACGT 597  
QY 541 GTTGAGAGTTGTGCTTTTGTGATTTGACATCCCTCGACATGTACTCTGGTATACACTTTAT 600  
Db 598 GTTGAGAGTTGTGCTTTTGTGATTTGACATCCCTCGACATGTACTCTGGTATACACTTTAT 657  
QY 601 TTGACGATAACAACTTTTTTTTCCCTCTACCTCTGATTTTGGTGTCTATATTTAATT 660  
Db 658 TTGACGATAACAACTTTTTTTTCCCTCTACCTCTGATTTTGGTGTCTATATTTAATT 717  
QY 661 TTATGCTATACCTGGGAGATGATCAACAGATAAGGATGCCAGATGCTCCATCCAGT 720  
Db 718 TTATGCTATACCTGGGAGATGATCAACAGATAAGGATGCCAGATGCTCCATCCAGT 777  
QY 721 GTACCAAAACAGAGAGTGTGAAGTTGACAAAGATGTGTGTGTGGTGTGTGTCTTT 780

Db 778 GTACCAAAACAGAGAGTGAAGTTGACAAAGATGGTCTGGTGTGTAGTCTTT 837  
Qy 781 ATCCCTGAGTGGCCCTTATCATGTGATACAACTGGTGAATCTACAGATGGAACAGGCC 840  
Db 838 ATCCCTGAGTGGCCCTTATCATGTGATACAACTGGTGAATCTACAGATGGAACAGGCC 897  
Qy 841 ACATGGCCCTTCTATGTGGTTATACCTCTCACTGTCTCAGTATGCCAGCAGCAGC 900  
Db 898 ACATGGCCCTTCTATGTGGTTATACCTCTCACTGTCTCAGTATGCCAGCAGCAGC 957  
Qy 901 ATTAACCCCTTCTCTACATCTGCTGAGTGGAAATTTCCAGAACGCTGCTCAATC 960  
Db 958 ATTAACCCCTTCTCTACATCTGCTGAGTGGAAATTTCCAGAACGCTGCTCAATC 1017  
Qy 961 CAAAGAAGAGCGACTGAGAAGGAATCAACAATATGGGAAACACTCTGAATACACATTT 1020  
Db 1018 CAAAGAAGAGCGACTGAGAAGGAATCAACAATATGGGAAACACTCTGAATACACATTT 1077  
Qy 1021 TAG 1023  
Db 1078 TAG 1080

RESULT 13  
AAF58619  
ID AAF58619 standard; cDNA; 1023 BP.  
XX AC AAF58619;  
XX DT 24-APR-2001 (first entry);  
XX DE Human AXOR21 nucleotide sequence.  
XX  
KW Human; AXOR21; G-protein coupled receptor; anorectic; antidiabetic;  
KW cytosolic; antiasthmatic; antiparkinsonian; cardiac; hypertensive;  
KW osteopathic; antiemetic; cerebroprotective; antidiabetic; antiallergic;  
KW antimitotic; antiemetic; tranquilizer; antitumor; gene therapy; vaccine;  
KW cancer; neurological disorder; ss.  
XX OS Homo sapiens.  
XX  
XX WO200107606-A1.  
XX PN  
XX PD 01-FEB-2001.  
XX  
XX PF 27-JUL-2000; 2000WO-GE002899.  
XX XX  
XX PR 27-JUL-1999; 99GB-00017627.  
XX PR 24-AUG-1999; 99GB-00020046.  
XX XX  
XX PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX PI Duckworth DM, Hill J, Muir AI, Szekeres PG;  
XX  
XX WPI; 2001-182790/18.  
XX DR  
XX DR P-PSDB; AAB68893.  
XX  
XX PT Novel G-protein coupled receptor polypeptide, AXOR21, useful for treating  
XX obesity, diabetes, eating disorders such as anorexia and bulimia,  
XX PT hypertension, osteoporosis, angina pectoris and myocardial infarction.  
XX  
XX PS Claim 4; Page 31; 42pp; English.  
XX  
XX CC The present sequence encodes AXOR21, a G-protein coupled receptor. AXOR21  
XX polynucleotides and polypeptides are useful for treating and diagnosing  
XX conditions such as pain, cancer, diabetes, obesity, anorexia, bulimia,  
XX CC asthma, Parkinson's disease, acute heart failure, hypotension,  
XX CC hypertension, urinary retention, osteoporosis, angina pectoris,  
XX CC myocardial infarction, stroke, ulcers, allergies, benign prostatic  
XX CC hypertrophy, migraine, vomiting, psychotic and neurological disorders  
XX including anxiety, schizophrenia, manic depression, depression, delirium,  
XX dementia and severe mental retardation, and dyskinesia such as

CC Huntington's disease or Gilles de la Tourette's syndrome. AXOR21  
CC polynucleotides and polypeptides are also useful for screening and  
CC structure based designing of antagonists, agonists and inhibitors of  
CC AXOR1. AXOR21 polynucleotides are useful for chromosome localization  
CC studies, as diagnostic reagents for detecting mutations in associated  
CC genes, and as valuable tools for tissue expression studies. AXOR21  
CC polynucleotides and polypeptides are useful as vaccines  
XX  
SQ Sequence 1023 BP; 264 A; 230 C; 222 G; 307 T; 0 U; 0 Other;  
XX  
Query Match 99.8%; Score 1021.4; DB 5; Length 1023;  
Best Local Similarity 99.9%; Pred. No. 5.6e-295;  
Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGAATCATTTTCATGATCTTTGTGGAACACCTCTCCGAACTTTTAAACAAATCTCTGG 60  
Db 1 ATGAATCATTTTCATGATCTTTGTGGAACACCTCTCCGAACTTTTAAACAAATCTCTGG 60  
Qy 61 AATAAAGAGTTTGTCTTATCAAACTGCCAGTGTGTAGATACAGTCACTCCCTTCCATG 120  
Db 61 AATAAAGAGTTTGTCTTATCAAACTGCCAGTGTGTAGATACAGTCACTCCCTTCCATG 120  
Qy 121 ATTGGGATTTCTTTCAACAGGGCTGGTTGGCAACATCTCTCATTTGATTACATATAATA 180  
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Dd	1021	TAG 1023 	
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ID	ABL41166 standard; DNA; 1023 BP.		
XX	AC ABL41166;		
XX	DE 12-AUG-2002 (first entry)		
XX	Human seven transmembrane receptor, 58875 protein coding sequence.		
KW	Human; seven transmembrane domain receptor; 65499; 58875; cytotstatic; osteopathic; vasotropic; cardiac; antiparkinsonian; antidiabetic; analgesic; neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic; antirheumatic; antiarthritic; anorectic; immunomodulator; gene therapy.		
OS	Homo sapiens.		
XX	OS		
FH	Key Location/Qualifiers		
FT	CDS 1..1023		
FT	/tag= a		
FT	/product= "58875 protein"		
XX	WO200228901-A2.		
XX	11-APR-2002.		
XX	03-OCT-2001; 2001WO-US031250.		
XX	05-OCT-2000; 2000US-0237700P.		
XX	(MILL-) MILLENNIUM PHARM INC.		
PA	Gluckmann MA;		
PI	WPI; 2002-444096/47.		
DR	P-PSDB; ABB07986.		
XX	Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane domain receptors, useful as reagents or targets for treatment or diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's disease, obesity.		
XX	Claim 1; Fig 8; 132pp; English.		
XX	The invention relates to novel seven transmembrane domain receptors, designated 65499 or 58875. The 65499 and 58875 polypeptides can be expressed by standard recombinant methodology. The polypeptides, encoding polynucleotides and modulators are useful for controlling G protein and coupled receptor-related disorders, and as a novel diagnostic target and therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated or related disorders such as cellular proliferative and differentiative disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism disorders (e.g., osteoporosis, rickets), haematopoietic disorders (such as chronic myelogenous leukemia, acute promyeloid leukemia), cardiovascular disorders (e.g., ischaemic heart disease, myocardial infarction, etc), endothelial cell disorder (e.g., psoriasis, Grave's disease), brain disorders (e.g., multiple sclerosis, Parkinson's disease), hormonal disorders (diabetes mellitus, hyperthyroidism), immune disorders (including autoimmune diseases such as rheumatoid disease).		



QY 901 ATTAAACCCCTTTCTCTACATCTGCTGAGTGGAAATTTCCAGAAACGTCCTGCTCAATC 960  
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 XX  
 AC ABL41165;  
 XX  
 DT 12-AUG-2002 (first entry)  
 XX  
 DE Human seven transmembrane receptor, 58875 protein encoding DNA.  
 XX  
 KW Human; seven transmembrane domain receptor; 65499; 58875; cytosolic;  
 KW osteopathic; vasotropic; caxdiant; antipsoriatic; antithyroid; gene; ds;  
 KW neuroprotective; antiparkinsonian; antidiabetic; virucide; analgesic;  
 KW antirheumatic; antiarthritic; anorectic; immunomodulator; gene therapy.  
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 FH Key  
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 FT /note= "the coding sequence (ABL41166) is specifically  
 claimed"

WO200228901-A2.  
 11-APR-2002.  
 03-OCT-2001; 2001WO-US031250.  
 05-OCT-2000; 2000US-0237700P.  
 (MILL-) MILLENNIUM PHARM INC.  
 Gluckmann MA;  
 WPI; 2002-444096/47.  
 P-PSDB; ABB07986.

Novel isolated 65499 or 58875 polypeptide, novel seven transmembrane domain receptors, useful as reagents or targets for treatment or diagnosis of rheumatoid arthritis, ischemic heart disease, Grave's disease, obesity.

Claim 2; Fig 8; 132pp; English.

The invention relates to novel seven transmembrane domain receptors, designated 65499 or 58875. The 65499 and 58875 polypeptides can be expressed by standard recombinant methodology. The polypeptides, encoding polynucleotides and modulators are useful for controlling G protein coupled receptor-related disorders, and as a novel diagnostic target and therapeutic agent in treatment and diagnosis of 65499 or 58875 mediated or related disorders such as cellular proliferative and differentiative disorders (including cancer e.g., carcinoma, sarcoma), bone metabolism disorders (including osteoporosis, rickets), haematopoietic disorders (such as chronic myelogenous leukemia, acute promyeloid leukemia), cardiovascular disorders (e.g., ischaemic heart disease, myocardial infarction, etc), endothelial cell disorder (e.g., psoriasis, Grave's disease), brain disorders (e.g., multiple sclerosis, Parkinson's disease), hormonal disorders (diabetes mellitus, hyperthyroidism),

CC immune disorders (including autoimmune diseases such as rheumatoid  
 CC arthritis, osteoarthritis), liver disorders, viral diseases such as  
 CC hepatocellular cancer, pain disorders (e.g., pain associated with surgery  
 CC or chest pain), metabolic disorders (obesity, cachexia),. The 65499 or  
 CC 58875 molecules are useful as surrogate markers, as pharmacodynamic  
 CC markers and as pharmacogenomic markers. The present sequence represents a  
 CC DNA encoding the human 58875 protein  
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 Query Match 99.8%; Score 1021.4; DB 6; Length 1278;  
 Best Local Similarity 99.9%; Pred. No. 6.2e-295;  
 Matches 1022; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Job time : 475 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1023	100.0	1023	6 AX665924	AX665924 Sequence
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5	1023	100.0	1023	6 BD097492	BD097492 Novel mel
6	1023	100.0	1023	6 BD141140	BD141140 Screening
7	1023	100.0	1023	9 AB058849	AB058849 Homo sapi
8	1023	100.0	1023	9 AY029596	AY029596 Homo sapi
9	1023	100.0	1035	6 BD141136	BD141136 Screening
10	1023	100.0	1035	6 AX230170	AX230170 Sequence
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DEFINITION Sequence 2 from patent US 6593108.  
ACCESSION AR353776  
VERSION AR353776.1 GI:33759828  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1023)  
AUTHORS Liu, Q., McDonald, T.P. and Howard, A.D.  
TITLE Nucleic acid molecule encoding a melanin-concentrating hormone  
receptor 2 polypeptide  
JOURNAL Patent: US 6593108-A 2 15-JUL-2003;

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VERSION	AX148198.1	GI:14347092	
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REFERENCE	Chen R., Dang H.T. and Lowitz K.P.		
AUTHORS	Endogenous and non-endogenous versions of human g protein-coupled		
TITLE	receptors		
JOURNAL	Patent: WO 0136471-A 35-MAY-2001;		
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Qy	601	TTGACGATAACAATTTTTCCTCTACCCCTGATTTGGTGGCTATATTTAAT	660
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LOCUS      1023 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Novel G protein-coupled receptor protein and DNA thereof.
ACCESSION BD003056
VERSION   1 GI:18631017
KEYWORDS  JP 2001017186-A/1.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1023)
AUTHORS   Watanabe,T., Terao,S. and Araya,Y.
TITLES    Novel G protein-coupled receptor protein and DNA thereof
JOURNAL   Patent: JP 2001017186-A 1 23-JAN-2001;
          TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT   OS Homo sapiens (human)
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          PD 23-JAN-2001
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LOCUS      1023 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Novel melanin-concentrating-hormone receptor.
ACCESSION BD097492
VERSION   1 GI:22643066
KEYWORDS  WO 0170975-A/1.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 1023)
AUTHORS   Kurama,T., Matsumoto,S., Takasaki,J., Matsumoto,M., Kamohara,M.,
          Saito,T., Oda,T. and Saito,Y.
TITLES    Novel melanin-concentrating-hormone receptor
JOURNAL   Patent: WO 0170975-A 1 27-SEP-2001;

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YAMANOUCHI PHARMACEUTICAL CO LTD,HELIX RESEARCH INSTITUTE, TAKESHI KURAMA, SHUNICHIRO MATSUMOTO,JUN TAKASAKI,MITSUYUKI MATSUMOTO, MASAZUMI KAMOHARA, TETSU SAITO,TAKAKI ODA,YOKO SAITO	FT
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PD 27-SEP-2001	
PF 23-MAR-2001 WO 2001JP002343	
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ACCESSION			BD141140	
VERSION			BD141140.1 GI:23236085	
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AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
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DEFINITION Homo sapiens mRNA for GPRv17, complete cds.  
 ACCESSION AB058849  
 VERSION AB058849.1  
 KEYWORDS GI:19910942  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 Kurama, T., Matsumoto, S., Takasaki, J., Terai, K., Matsumoto, M., Kanohara, M., Saito, T., Soga, T., Saito, Y., Oda, T., Masuho, Y. and Furuichi, K.  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Molecular characterization of a novel melanin-concentrating hormone receptor: Evidence of its expression in lateral hypothalamus

JOURNAL Unpublished  
 AUTHORS Kurama, T., Matsumoto, S. and Takasaki, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-MAR-2001) Takeshi Kurama, Yamanouchi Pharmaceutical Co., Ltd., Institute for Drug Discovery Research, 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan (E-mail: kurama@yamanouchi.co.jp, Tel: 81-298-54-1636, Fax: 81-298-52-5412)

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DEFINITION Homo sapiens melanin-concentrating hormone 2 receptor mRNA,
complete cds.
ACCESSION AY029596
VERSION AY029596.1 GI:14388165
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Sailer,A.W., Sano,H., Zeng,Z., McDonald,T.P., Pan,J., Pong,S.-S.,
Feighner,S.D., Tan,C.P., Fukami,T., Iwaasa,H., Hreniuk,D.L.,
Morin,N.R., Sadowski,S.J., Ito,M., Ito,M., Bansal,A., Ky,B.,
Figuerola,D.J., Jiang,Q., Austin,C.P., MacNeil,D.J., Ishihara,A.,
Ihara,M., Kanatani,A., Van der Ploeg,L.H.T., Howard,A.D. and Liu,Q.
Identification and characterization of a second
melanin-concentrating hormone receptor, MCH-2R
Proc. Natl. Acad. Sci. U.S.A. 98 (13), 7564-7569 (2001)
21309932
PUBMED 1140457
REFERENCE 2 (bases 1 to 1023)
AUTHORS Sailer,A.W., Sano,H., Zeng,Z., McDonald,T.P., Pan,J., Pong,S.-S.,

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Feighner,S.D., Tan,C.P., Fukami,T., Iwaasa,H., Hreniuk,D.L.,
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Figuerola,D.J., Jiang,Q., Austin,C.P., MacNeil,D.J., Ishihara,A.,
Ihara,M., Kanatani,A., Van der Ploeg,L.H.T., Howard,A.D. and Liu,Q.
Direct Submission
Submitted (10-APR-2001) Metabolic Disorders, Merck & Co., Inc., 126
E. Lincoln Av., RY80V-265, Rahway, NJ 07065, USA
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Best Local Similarity 100.0%; Pred. No. 8,7e-274;
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ACCESSION BD141136
VERSION BD141136.1 GI:23236081
KEYWORDS WO 0203070-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Mori, M., Shimomura, Y., Harada, M., Sugo, T. and Shintani, Y.
TITLE Screening method for MCH receptor antagonist or agonist
JOURNAL Patent: WO 0203070-A 3 10-JAN-2002;
TAKEDA CHEMICAL INDUSTRIES LTD./MASAOKI MORI, YUKIO SHIMOMURA, MIKO
HARADA, TSUKASA SUGO, YASUSHI SHINTANI
COMMENT OS Homo sapiens (human)
PN WO 0203070-A/3
PD 10-JAN-2002
PF 04-JUL-2001 WO 2001JP005809
PR 05-JUL-2000 JP OOP 208254
PI MASAOKI MORI, YUKIO SHIMOMURA, MIKO HARADA, TSUKASA SUGO, YASUSHI

PI SHINTANI
PC GOIN33/566, GOIN33/50, GOIN33/15
CC Screening method for MCH receptor antagonist or agonist. FH
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Best Local Similarity 100.0%; Pred. No. 8.7e-274;
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 57 from Patent WO0162797.
ACCESSION
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VERSION
AX230170.1 GI:15592188
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Vogeli, G., Wood, L.S., Parodi, L.A. and Lind, P.
Novel g protein-coupled receptors
Patent: WO 0162797-A 57 30-AUG-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Best Local Similarity 100.0%; Pred. No. 8.5e-274;
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LOCUS
DEFINITION
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to Homo sapiens slt mRNA for G protein-coupled receptor.
ACCESSION
AK123634
VERSION
AK123634.1 GI:34529233
KEYWORDS
oligo capping; f1s (full insert sequence).
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Tanigami, A., Fujiwara, T., Shibahara, T., Goto, Y., Hirao, M.,
Shimizu, F., Wakebe, H., Ono, T., Hishigaki, H., Watanabe, T., Ozaki, K.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
NEO human cDNA sequencing project
Unpublished
2 (bases 1 to 2368)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI); supported by Japan
Key Technology Center etc.; 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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DEFINITION Sequence 1 from Patent WO0107606.
ACCESSION AX077691
VERSION AX077691.1 GI:13122068
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Duckworth, D.M., Hill, J.S., Muir, A.I. and Szekeres, P.G.
TITLE Axor21, a G-protein coupled receptor
JOURNAL Patent: WO 0107606-A 1 01-FEB-2001;
SMITHKLINE BEECHAM PLC (GB)
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Best Local Similarity 99.9%; Pred. No. 2.4e-273;
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ACCESSION	AX459698		
VERSION	AX459698.1 GI:21725545		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Gluckmann, M.A.		
TITLE	65499 and 58875, novel seven-transmembrane receptors and uses therefor		
JOURNAL	Patent: WO 0228901-A 6 11-APR-2002;		
FEATURES	Millennium Pharmaceuticals, Inc. (US)		
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ACCESSION	AF399937		
VERSION	AF399937.1 GI:15667842		
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ORGANISM	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1023)

Wang, S., Behan, J., O'Neill, K., Weig, B., Fried, S., Laz, T., Bayne, M., Gustafson, E. and Hawes, B.E. Identification and pharmacological characterization of a novel human melanin-concentrating hormone receptor, mch-r2 J. Biol. Chem. 276 (37), 34664-34670 (2001)

21433376 PUBMED 11459838

REFERENCE 2 (bases 1 to 1023)

Wang, S., Behan, J., Fried, S., Hawes, B. and Laz, T. Direct Submission

TITLE Submitted (12-JUL-2001) Human Genomics/CNS, Schering-Plough Res Inst, 2015 Galloping Hill Rd, Kenilworth, NJ 07033, USA

JOURNAL Location/Qualifiers

FEATURES source

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LOCUS 1278 bp DNA linear PAT 08-JUL-2002

DEFINITION Sequence 3 from Patent WO2228901.

ACCESSION AX459695

VERSION AX459695.1 GI:21725542

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Gluckmann, M.A.

TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

JOURNAL Patent: WO 0228901-A 3 11-APR-2002; Millennium Pharmaceuticals, Inc. (US)

FEATURES source

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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15	130.4	12.7	1385	3	US-08-984-288-1
16	130.4	12.7	3488	4	US-09-218-467B-1
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20	82.8	8.1	1000	3	US-08-147-592A-11
21	82.8	8.1	1000	4	US-08-292-694A-11
22	82.2	8.0	1334	4	US-09-761-962A-3
23	82.2	8.0	1365	4	US-09-761-962A-11
24	82.2	8.0	1423	4	US-09-761-962A-1
25	82.2	8.0	1342	4	US-09-761-962A-1
26	82.2	8.0	1610	4	US-09-761-962A-16
27	82.2	8.0	1729	4	US-09-761-962A-9

28 82.2 8.0 2045 4 US-09-761-962A-10 Sequence 10, Appl  
29 79.4 7.8 1408 4 US-09-214-904-5 Sequence 5, Appl  
30 79.4 7.8 1410 3 US-08-147-592A-1 Sequence 1, Appl  
31 79.4 7.8 1410 4 US-08-292-694A-1 Sequence 1, Appl  
32 79.2 7.7 1142 3 US-08-765-743-1 Sequence 1, Appl  
33 79.2 7.7 1143 4 US-09-341-446B-1 Sequence 1, Appl  
34 79.2 7.7 1284 4 US-09-341-446B-3 Sequence 3, Appl  
35 79 7.7 1147 1 US-08-417-103-15 Sequence 15, Appl  
36 79 7.7 1351 1 US-07-816-283-5 Sequence 5, Appl  
37 79 7.7 1351 4 US-09-016-434-1303 Sequence 1303, Ap  
38 78.6 7.7 1296 1 US-07-816-283-9 Sequence 9, Appl  
39 78.6 7.7 1296 1 US-08-417-103-9 Sequence 9, Appl  
40 78.6 7.7 1413 4 US-09-016-434-1321 Sequence 1321, Ap  
41 78.6 7.6 1618 3 US-08-889-108-1 Sequence 1, Appl  
42 77.8 7.6 1618 3 US-08-889-108-3 Sequence 3, Appl  
43 77.8 7.6 1618 3 US-08-120-601B-1 Sequence 1, Appl  
44 77.8 7.6 1618 3 US-08-120-601B-3 Sequence 3, Appl  
45 77.8 7.6 1618 3 US-08-120-601B-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-712-368-2  
; Sequence 2, Application US/09712368  
; Patent No. 6593108  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Qingyun  
; APPLICANT: McDonald, Terrence P.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Iwaasa, Hisashi  
; APPLICANT: Sano, Hideki  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: 20579Y  
; CURRENT APPLICATION NUMBER: US/09/712.368  
; CURRENT FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: 60/165,871  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 60/188,977  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/198,029  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1023  
; TYPE: DNA  
; ORGANISM: Human  
US-09-712-368-2

Query Match 100.0%; Score 1023; DB 4; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1023; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAATCCATTTCGATCTTTGTTGGAACACCTCTCGGAACTTTTAAACAAATCTGG 60  
Db 1 ATGAATCCATTTCGATCTTTGTTGGAACACCTCTCGGAACTTTTAAACAAATCTGG 60  
QY 61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCTCCCTCCATG 120  
Db 61 AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCTCCCTCCATG 120  
QY 121 ATTGGGATTATCTTTCAACAGGGCTGGTTGGCAACATCTCTATTGTATTCACTATAATA 180  
Db 121 ATTGGGATTATCTTTCAACAGGGCTGGTTGGCAACATCTCTATTGTATTCACTATAATA 180  
QY 181 AGATCCAGGAAAAAAGACGTCCTTGACATCTATATCTGCAACCTGGCTGTGCTGATTG 240  
Db 181 AGATCCAGGAAAAAAGACGTCCTTGACATCTATATCTGCAACCTGGCTGTGCTGATTG 240  
QY 241 GTCCACATAGTTGAATGCCCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGTG 300  
Db 241 GTCCACATAGTTGAATGCCCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGTG 300

Db 241 GTCCACATAGTTCGAATGCTTTTCTTATTACCAATGGGCCCGAGGGGAGAGTGGGTG 300  
Qy 301 TTTGGGGGGCTCTGCGACATCATACATCCCTGGATACCTGTAAACCAATTTGCTCT 360  
Db 301 TTTGGGGGGCTCTGCGACATCATACATCCCTGGATACCTGTAAACCAATTTGCTCT 360  
Qy 361 AGTGCCATCATGACTGTAATGATGAGTGGACAGTACTTTGGCCCTCTGCAACATTTGCA 420  
Db 361 AGTGCCATCATGACTGTAATGATGAGTGGACAGTACTTTGGCCCTCTGCAACATTTGCA 420  
Qy 421 CTGACAGCTTTGGAGAACAGGATACAGACCATCCGATCAATTTGGCCCTTTGGGCGAGCT 480  
Db 421 CTGACAGCTTTGGAGAACAGGATACAGACCATCCGATCAATTTGGCCCTTTGGGCGAGCT 480  
Qy 481 TCCTTTATCTGCGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 TCCTTTATCTGCGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Qy 541 GTTGAGAGTTGCTTTGATTTGACATCCCTGACGATGACTCTGCTGATACACTTTAT 600  
Db 541 GTTGAGAGTTGCTTTGATTTGACATCCCTGACGATGACTCTGCTGATACACTTTAT 600  
Qy 601 TTGACGATACAACTTTTTTTTTTCCCTCTACCTTGTATTTGGTGTGCTATATTTAAAT 660  
Db 601 TTGACGATACAACTTTTTTTTTTCCCTCTACCTTGTATTTGGTGTGCTATATTTAAAT 660  
Qy 661 TTATGCTATATTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT 720  
Db 661 TTATGCTATATTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCAGT 720  
Qy 721 GTACCAAAACAGAGATGATCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 GTACCAAAACAGAGATGATCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Qy 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Db 781 ATCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Qy 841 ACATGCGCTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 ACATGCGCTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Qy 901 ATTAACCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGCTGCTGCTCAATC 960  
Db 901 ATTAACCTTTTCTCTACATCCTGCTGAGTGGAAATTTCCAGAAACGCTGCTGCTCAATC 960  
Qy 961 CAAGAAGAGGAGTGGAGGAAATCAACATATGGAACACTCTGAAATCACACTTT 1020  
Db 961 CAAGAAGAGGAGTGGAGGAAATCAACATATGGAACACTCTGAAATCACACTTT 1020  
Qy 1021 TAG 1023  
Db 1021 TAG 1023

RESULT 2  
US-09-712-368-3/c  
; Sequence 3, Application US/09712368  
; Patent No. 6593108  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Qingyun  
; APPLICANT: McDonald, Terrence P.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Iwasa, Hisashi  
; APPLICANT: Sano, Hideki  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: 20579Y  
; CURRENT APPLICATION NUMBER: US/09/712,368  
; CURRENT FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: 60/165,871  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 60/188,977  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 60/188,977  
; PRIOR FILING DATE: 2000-03-13

; PRIOR APPLICATION NUMBER: 60/198,029  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 925  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(925)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-712-368-3  
  
Query Match 21.1%; Score 215.4; DB 4; Length 925;  
Best Local Similarity 99.5%; Pred. No. 3.8e-59;  
Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 179 TAAGATCCAGGAAAAAACAAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 238  
Db 534 TCAGATCCAGGAAAAAACAAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATT 475  
Qy 239 TGGTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCCGAGGGAGAGTGGG 298  
Db 474 TGGTCCACATAGTTGGAATGCTTTTCTTATTCACCAATGGCCCGAGGGAGAGTGGG 415  
Qy 299 TGGTGGGGGGCTCTCTGACCAATCATCATCCCTGGATCTTTGAACCAATTTGCTCT 358  
Db 414 TGGTGGGGGGCTCTCTGACCAATCATCATCCCTGGATCTTTGAACCAATTTGCTCT 355  
Qy 359 GTAGTGCCATCATGCTCTTAATAGTGTGGACAGTA 395  
Db 354 GTAGTGCCATCATGCTCTTAATAGTGTGGACAGTA 318

RESULT 3  
US-09-712-368-4  
; Sequence 4, Application US/09712368  
; Patent No. 6593108  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Qingyun  
; APPLICANT: McDonald, Terrence P.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Iwasa, Hisashi  
; APPLICANT: Sano, Hideki  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: 20579Y  
; CURRENT APPLICATION NUMBER: US/09/712,368  
; CURRENT FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: 60/165,871  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 60/188,977  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/198,029  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 925  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(925)  
; OTHER INFORMATION: n = A,T,C or G  
; OTHER INFORMATION: Antisense sequence of Sequence ID. No. 6593108 3  
; Patent No. 6593108  
US-09-712-368-4

Query Match 21.1%; Score 215.4; DB 4; Length 925;  
Best Local Similarity 99.5%; Pred. No. 3.8e-59;  
Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Db	264	TCATCATCAACCTCTCTGTGGTGAATCTGCTTCTCTGCTGGGCAAGCCCTTTCAATGATCC	323
Qy	272	ACCAATGGGCCCCGAGGGGGAGAGTGGGTGTTTGGGGGGCCTCTCTGACACCATCATCACAT	331
Db	324	ACCAGCTCATGGGGAACGGCGTCTGGGCACATTGGGGHAAACAATGTGCACCTCATCACAG	383
Qy	332	CCCTGGATATTTGTAAACAAATTTGCCCTGTAGTGCCATCATGACTGTAATGAGTGTGAACA	391
Db	384	CCATGGACGCCAACAGTCAGTTCACTAGCACCTACATCCTGACTGCCATGACCATTCGACC	443
Qy	392	GGTACTTTGGCCTCGTCCAAACCAATTCGAGCTGCACCGTTGGAGAACAAAGGTACAAGACCA	451
Db	444	GCTACTTTGGGCACCGTCCACCCCATCTCTCCACAAGTTCCGGAAGCCCTCCATGGCCA	503
Qy	452	TCGGGATCAATTTGGGCGCTTTGGGCGAGCTTCCTTTATCCTGGCATTCGCCCTGTCTGGGTCT	511
Db	504	CCCTGGTGAATCGCTCCTGTGGGCGCTCTCCTTCATCAGTATCACCCCTGTGTGGCTCT	563
Qy	512	ACTCGAAGGTCAATCAAAATTTAAGACGGGTGTGAGATGTGTGCTTTTGATTTGACATCCC	571
Db	564	ACGCCAGGCTCAATCCCTTCCACGGGGGTGTGTGGCTGTGGCATCCGCTTGCACAAACC	623
Qy	572	CTGACGATGTACTCTGTGTATACACTTATTGTGACGATAACAACCTTTTTTTTCCCTCTAC	631
Db	624	CGGACACTGACCTCT-----ACTGGTCACTCTGTACACAGTTTTTCTGGCCCTTTGCC	676
Qy	632	CCTTGATTTTGGTGTGTATATTTAAATTTTATGCTATACTTGGGAGATGTATCAACAGA	691
Db	677	CTTCCGTTTGTGGTCAATTACCGCGCATACGTGAAATACTACAGCGCATGAC-----GT	731
Qy	692	ATAAGGATGCCAGATGTGCAATCCCAAGTGTACCAAAACAGAGAGTGAATGAGTTGACAA	751
Db	732	CTTCGGTGGGCCACGACCTCCCAACGCGAGCATCCGGCTTCGGACA---AAGAGGGGTGACC	789
Qy	752	AGATGGTCTGGTCTGGTGGTAGTCTTTATCCTGAGTGTGCCCTTATCATGTGATAC	811
Db	789	GCACGGCCATTGCCATCTGTCTGTCTTTCTTTGTGTGCTGGGACCTACTATGTGTCTGC	848
Qy	812	AACTGTGTAACTTACAGATGGAACAGCCCCACACTGGCCTTCTATGTGGGTTATTACCTCT	871
Db	849	AGCTGACCCAGCTGTCCATCAGCGCGCGACCCCTCACGTTTGTCTACTTGTACAAACGGG	908
Qy	872	CCATCTGTCTCAGTATGCCAGCAGCAGCATTAACCTTTTCTCTACATCCTGCTGAGTG	931
Db	909	CCATCAGCTTGGGCTATGCTAACAGCTGCCTGAAACCCCTTTGTGTAGTACTGCTCTGTG	968
Qy	932	GAATAATTCAGAAACGTCCTGCTCAAAATCCAAAGAACAGCGACCTGAGAAAGGAATCAACA	991
Db	969	AGACCTTTCGNAACCGCTTGGTGTGTGTCAGTGAAGCCTGCAGGCCAGGGCAGCTCCGCA	1028
Qy	992	ATATGGAAACACTCTGAATC	1013
Db	1029	CGGTCAACACGCTCAGACAGC	1050

RESIT, T. 6

RESULT 6  
 US-09/478-602-3  
 ; Sequence 3, Application US/09478602  
 ; Patent No. 6291195  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Salton, John A.  
 ; APPLICANT: Laz, Thomas M.  
 ; APPLICANT: Ngornay, Raisa  
 ; APPLICANT: Wilson, Amy E.  
 ; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone  
 ; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof  
 ; FILE REFERENCE: 57453Y/JPW  
 ; CURRENT APPLICATION NUMBER: US/09/478,602  
 ; CURRENT FILING DATE: 2000-01-06  
 ; EARLIER APPLICATION NUMBER: 09/224,426  
 ; EARLIER FILING DATE: 1998-12-31  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.1

RESULT 7  
US-09-218-467B-6  
; Sequence 6, Application US/09218467B  
; Patent No. 6362326  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH  
; APPLICANT: ELLIS, CATHERINE  
; APPLICANT: HALSEY, WENDY  
; APPLICANT: BERGSMAN, DEK  
; TITLE OF INVENTION: 11cby Genomic Sequence  
; FILE REFERENCE: GP-50010  
; CURRENT APPLICATION NUMBER: US/09/218,467B  
; CURRENT FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 980  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
US-09-218-467B-6

Query Match 12.7%; Score 130.4; DB 4; Length 980;  
Best Local Similarity 50.1%; Pred. No. 9,7e-32;  
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;

QY	186	CAGGAAAAAAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTGGTCCA	245
DB	134	CTGGTCGACACGCTCCCGACATCTTCATCAACCTCTCGGTAGTAGTCTCTCTT	193
QY	246	CATAGTTGGAAATGCTTTCTTATTCACCAATGGGCGGAGGGGAGTGGGTGTTGG	305
DB	194	TCTCCTGGGATGCCCTTCATGATCCACCACTGATGGCAATGGGTGGACATTGG	253
QY	306	GGGGCTCTCTGACCATCATCATCTCCCTGGTACTTGAACCAATTTGCTGTAGTGC	365
DB	254	GGAGCAATGTGACCTCATCAACGCGCATGGATGCAATAGTCAGTCCACGACCTA	313
QY	366	CATCATGACTGTAAATGAGTGTGACAGTACTTTGGCCCTGCTCCCAACCAATTCG	425
DB	314	CATCCTGACCGCATGGCATTGACCGTACCTGCGCCACTGCCACCCCATCTCTCC	373
QY	426	ACGTTGGAGAACAGGTACAGACCATCGGATCAATTTGGGCTTTGGGAGCTCTCT	485
DB	374	GAAGTTCCGGAAGCCCTGTGTGGCCACCTGGTGTGATCTGCTCTGGGCGCTCT	433
QY	486	TATCCTGGCATTCGCTGTCTGGGTCTACTCGAAGGTCAATCAATTTAAAGACG	545
DB	434	CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCAGAGGTGC	493
QY	546	GAGTTGTGCTTTGATTTGACATCCCTCGACGATGACTCTGTGTATACATTTAT	605
DB	494	GGCTCGGCGATACGGCTGCGCAACCCAGACACTGACCTCT-----ACTGGT	545
QY	606	GATAAACAATTTTTTCCCTACCTTGAATTTGGTGTGCTATATTTAATTTATG	665
DB	546	CTGTACAGTTTTCCTGGCTTTGCGCTGCTTTTGTGGTATACACCGGATACG	605
QY	666	CTATATCTGGGAGATGTATCAACAGAAATAGGATGCCAGATGTGCAATCCAG	725
DB	606	AGGATCTGCGCGATGAGTCTCTCA-----GTGGCGCGCGCTCCAGCGAGAT	661
QY	726	AAACAGAGAGTATGAGTTGACAAAGATGGTGTGGTGTGGTGTATCTTTATCT	785
DB	662	GCTGCGGACA---AAGAGGTGACCGCGACAGCATCGCCATCTGTCTGTCTT	718
QY	786	GAGTGTGCGCCCTTATCATGTGATACAACTGGTGAATCTACAGATGGAACAG	845
DB	719	GTCTGGGACCTCTACTATGTGTACAGTACCCAGTTGTCCATCAGCGCGCGAC	778
QY	846	GGCTTCTATGTGGGTATTAATCTCTCCATCTCTCAGCTATGCCAGGAGCATTA	905

DB 779 CACCTTTGCTTACTTATACAAATGGCGCATCAGCTTGGGCTATGCAACAGCTGCTCAA 838

QY 906 CCGTTTCTCTACATCTCTGCTGAGTGGAAATTTCCAGAAACGCTGCTGCTCAAAATCCAAAG 965

DB 839 CCGCTTTGTGTACATCTGCTGCTGAGACGTTCCGAAACGCTTGGTCTCTGTCGGTGAA 898

QY 966 AAGAGCGACTGAGAAGAAATCAACAATATATGGGAAACACTCTGA 1009

DB 899 GCCTGCAGCCCGGGGAGCTTCGGCTGTGTACGACACGCTCAGA 942

RESULT 8  
US-09-170-496D-51  
; Sequence 51, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 51  
; LENGTH: 1209  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-170-496D-51

Query Match 12.7%; Score 130.4; DB 4; Length 1209;  
Best Local Similarity 50.1%; Pred. No. 1.1e-31;  
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;

QY	186	CAGGAAAAAAGTCCCTGACATCTATATCTGCAACCTGGCTGGCTGATTGGTCCA	245
DB	363	CTGTGTCACAAACGTCGCCGACATCTTCATCATCAACCTCTCGGTAGTAGTCTCTCT	422
QY	246	CATAGTTGGAAATGCTTTCTTATTCACCAATGGGCGGAGGGGAGTGGGTGTTGG	305
DB	423	TCTCCTGGCATGCCCTTCATGATCCACCACTCATGGCAATGGGTGGCACTTTGG	482
QY	306	GGGGCTCTCTGACCAATCATCATCTCTGATCTTTGATCAACAAATTTGCTGTAGTGC	365
DB	483	GGAGACCATGTGCACTCCCTCATCAGGGCATGGATGCAATAGTCAGTCCACGACCTA	542
QY	366	CATCATGACTGTAAATGAGTGTGACAGTACTTTGGCCCTGCTCCCAACCAATTCG	425
DB	543	CATCTGACCGCATGGCATTGACCGTACTCTGCGCACATGTCACCCCATCTCTTCC	602
QY	426	ACGTTGGAGAACAGGTACAGACCATCCGATCAATTTGGGCTTTGGGAGCTTCTCT	485
DB	603	GAAGTTCCGGAAGCCCTCTGTGGCGCACCTGTGTGATCTGCTCTGTGGGCGCTCT	662
QY	486	TATCCTGGCATTCGCTGTGCTGGTCTACTCGAAGGTCAATCAATTTAAAGACG	545
DB	663	CATCAGCATCACCCCTGTGTGGCTGTATGCGAGACTCATCCCTTCCAGAGGTGC	722
QY	546	GAGTTGTGCTTTGATTTGACATCCCTGACAGTGTACTCTGTGTATACATTTATTT	605
DB	723	GGGCTGGGCATACGCTGCCCAACCCAGACACTGACCTCT-----ACTGGTTC	774
QY	606	GATAAACAATTTTTTCCCTTACCTTGAATTTGGTGTGCTATATTTAATTTATG	665
DB	775	CTGTACCAAGTTTTCCTGGCGCTTTGCGCTGCTTTTGTGGTTCATCAGCGCG	834
QY	666	CTATATCTGGGAGATGTATCAACAGAAATAGGATGCCAGATGTGCAATCCAG	725
DB	835	AGGATCTGCGAGCGATGAGTCTCTCA-----GTGGCGCGCGCTCCAGCGAG	890
QY	726	AAACAGAGAGTATGAGTTGACAAAGATGGTGTGCTGTGTGTGTATCTTTATCT	785

Db 891 GCTGGGACA--AAGAGGTGACCGCACAGCCATCGCCATCTGCTCTCTTTGT 947  
Qy 786 GAGTGTGCCCCCTATCATGTGATACACTGGTGAACCTACAGATGAACAGCCCACT 845  
Db 948 GTGCTGGGACCCCTACTATGTGTACAGCTGACCCAGTGTGTCATCAGCGCCGACCT 1007  
Qy 846 GGCCTTCTATGTGGTATTACCTCTCCATCTGTCTCAGCTATGCCAGCAGCAGATTAA 905  
Db 1008 CACCTTTGTCTATTATACATCGGCCATCAGCTTGGGCTAIGCCAAAGCTGCTCAA 1067  
Qy 906 CCGTTTCTCTATCCTGTGTGGAATTTCCAGAAAGCTCTGCTCAAAATCCAAAG 965  
Db 1068 CCGCTTGTGTATCCTGTGTGAGACGTTCCGCAACGCTTGGTCTCTGCTGGTGA 1127  
Qy 966 AAGAGCGACTGAGAAGAAATCAACATATGGAACACACTCTGA 1009  
Db 1128 GCCTGCAGCCAGGGGAGCTTCGGCTGTGAGAAAGCTCAGA 1171

## RESULT 9

US-09-170-496D-191

; Sequence 191, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-

; TITLE OF INVENTION: Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 191

; LENGTH: 1209

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-170-496D-191

Query Match 12.7%; Score 130.4; DB 4; Length 1209;  
Best Local Similarity 50.1%; Pred. No. 1.1e-31;  
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;

Qy 186 CAGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGGTGTGCTGATTTGTTCCA 245  
Db 363 CTGTGCAACAACGCTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCTT 422  
Qy 246 CATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTGTTGG 305  
Db 423 TCTCTGGGATGCGCTTCTATGATCCACAGCTCATGGGCAATGGGTGGCACTTTGG 482  
Qy 306 GGGGCTCTCTGACCAATCATCATCCCTGGATCTGTAAACAATTTGCTGTGTAGTGC 365  
Db 483 GGAGACCATGTGCAACCTCATACGGCCATGGATGCCAATAGTCAGTTCACCAACCTTA 542  
Qy 366 CATCATGACTGTAATGAGTGGGACAGGTACTTTGCTCGTCCCAACCATTTTCACTGAC 425  
Db 543 CATCTGACCGCCATGGCCATTTGACCGCTACCTGGCCATCTGTCCTGTCCTCTCTCC 602  
Qy 426 ACCTTGGAGAACAGGTACAGACCATTCGGATCAATTTGGGCTTTTGGGACGTTTCTT 485  
Db 603 GAAGTTCGGAGAGCCCTCTGTGGCCACCTCTGGTGTATCTGCTCTGTGGCCCTCTCTT 662  
Qy 486 TATCTGGCATGCTCTCTGGGTCTACTCGAAGTTCATCAATTTAAAGACGGTGTGA 545  
Db 663 CATCAGCATCACCCCTGTGTGGTGTATGCCAGACTCATCCCTTCCCGAGAGGTGAGT 722  
Qy 546 GAGTGTGCTTTTGTATTTGATATCCCTGACGATGTACTCTGTGTATACATTTTATTGAC 605  
Db 723 GGGCTGGGCATAGCCTGCCCACACCCAGACACTGACCTCT-----ACTGTTTCAAC 774

Qy 606 GATAACAACCTTTTTTCCCTTACCTTGANTTTGGTGTGTATATTTTAAATTTATG 665  
Db 775 CTGTACCAAGTTTTTCTGGCCCTTTGGCCTTTTGTGTGTGTATCATCAGCGCATACGTG 834  
Qy 666 CTATACTTGGAGATGTATCAACAGATAAGGATGCCAGATGCTGCAATCCCACTGTACC 725  
Db 835 AGGATCTTGCAGGCGATGAGCTCTCA-----GTGGCCCGCCCTCCAGCGGCGCATCCG 890  
Qy 726 AAAACAGAGAGTGAAGTTGACAAAGATGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 785  
Db 891 GCTGCGGACA--AAGAGGTGAAACGACAGCCATGCCATCTGTCTGTCTCTCTTTGT 947  
Qy 786 GAGTGTGCCCCCTTATCATGTGATACAACTGCTGAACTTACAGATGAAACAGCCCACT 845  
Db 948 GTGCTGGGACCCCTACTATGTGTGACAGCTGACCCAGTGTGTCATCAGCGCCGACCT 1007  
Qy 846 GGCCTTCTATGTGGTATTATACCTCTGCATCTGTCTCAGCTATGCCAGCAGCAGCATTA 905  
Db 1008 CACCTTTGTCTATTATACATCGGCCATCAGCTTGGGCTAIGCCAAAGCTGCTCAA 1067  
Qy 906 CCGTTTCTCTATCCTGTGTGGAATTTCCAGAAAGCTCTGCTCAAAATCCAAAG 965  
Db 1068 CCGCTTGTGTATCCTGTGTGAGACGTTCCGCAACGCTTGGTCTCTGCTGGTGA 1127  
Qy 966 AAGAGCGACTGAGAAGAAATCAACATATGGAACACACTCTGA 1009  
Db 1128 GCCTGCAGCCAGGGGAGCTTCGGCTGTGAGAAAGCTCAGA 1171

## RESULT 10

US-09-224-426-1

; Sequence 1, Application US/09224426

; Patent No. 6221613

; GENERAL INFORMATION:

; APPLICANT: Salen, John A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Nagorny, Raisa

; APPLICANT: Wilson, Amy E.

; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone

; FILE REFERENCE: 57453/JPW/JHB

; CURRENT APPLICATION NUMBER: US/09/224,426

; CURRENT FILING DATE: 1998-12-31

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0 - beta

; SEQ ID NO 1

; LENGTH: 1269

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-224-426-1

Query Match 12.7%; Score 130.4; DB 3; Length 1269;  
Best Local Similarity 50.1%; Pred. No. 1.1e-31;  
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;

Qy 186 CAGAAAAAAGAGTCCCTGACATCTATATCTGCAACCTGGCTGTGCTGATTTGTTCCA 245  
Db 423 CTGTGCAACAACGCTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCTT 482  
Qy 246 CATAGTTGGAATGCTTTTCTTATTCACCAATGGCCGAGGGGAGAGTGGGTGTTGG 305  
Db 483 TCTCTGGGATGCGCTTCTATGATCCACAGCTCATGTCACAGCTCATGGGCAATGGGTGGCACTTTGG 542  
Qy 306 GGGGCTCTCTGACCAATCATCATCCCTGGATCTGTAAACAATTTGCTGTGTAGTGC 365  
Db 543 GGAGACCATGTGCAACCTCATACGGCCATGGATGCCAATAGTCAGTTCACCAACCTTA 602  
Qy 366 CATCATGACTGTAATGAGTGGGACAGGTACTTTGCTCGTCCCAACCATTTCCACTGAC 425  
Db 603 CATCTGACCGCCATGGCCATTTGACCGCTACTCTGCGCACTGTCCACCCCACTCTCTTCC 662  
Qy 426 ACCTTGGAGAACAGGTACAGACCATTCGGATCAATTTGGGCTTTTGGGACGTTTCTT 485

563	DB	GAAGTTCGGGAAGCCCTCTGTGGCCACCCCTGGTGATCTGCCTCTGTGGGCCCTCTGCCTT	722
486	QY	TATCTCTGGCATTCGCCCTGTCTGGGTCTACTCGAAGGTCATCAAAATTTAAAGACGGTGTGA	545
723	DB	CATCAGCATCACCCCTGTGTGGTGTATGCCAGACTCATCCCCTTCCAGGAGGTGCAGT	782
546	QY	GAGTCTGTCTTTTGATTTTGACATCCCTGACAGATGTACTCTGTGTATACACTTTTATTGAC	605
783	DB	GGGCTGGGCATACGGCTGCCAACCCAGACATGACCTCT-----ACTGGTTCAACC	834
606	QY	GATAACAACTTTTTTTTCCCTCTACGCCCTTGATTTTGGTGTGTATATTTTAAATTTATG	665
835	DB	CTGTACAGATTTTCTCGGCTTTTGGCCCTGCCCTTTTGTGTCTATCAGCGCGATACGTG	894
666	QY	CTATACTTGGGAGATGTATCAACAGAAATAGGATGCCAGATGCTGCAATCCCAAGTGTACC	725
895	DB	AGGATCTTCGACGGCATGAGCTCTCA----GTGGCCCCGCCCTCCAGCGCAGCATCCG	950
726	QY	AAACAGAGAGTGAAGAGTTGACAAAGATGGTGTGGTCTGGTGGTAGTCTTTTATCCCT	785
951	DB	GCTGCGGACA--AAGAGGGTGAACCCGCGACAGGCATCGCCATCTGTCTGTCTCTTTGT	1007
786	QY	GAGTGTGCCCCCTTATCATGTGATACAACTGGTGAATTAACAGATGGAACAGGCCCACT	845
1008	DB	GTGCTGGGCACCTCTAATGTGTCTACAGTGAACCCAGTGTCCATCAGCGCCCGACCTT	1067
846	QY	GGCCTTCTAATGTGGGTTATTAACCTCTCCATCTGTCTCAGTATGCCAGCAGCAGCATTA	905
1068	DB	CACCTTTGTCTACTTATACAATGGGCCATCAGCTTGGGTATGCCAACAGCTGSCCTCA	1127
906	QY	CCCTTTTCTCTACATCTCTGTGAGTGGAAATTTCCAGAAACGTCCTGCTCAAAATCCAAAG	965
1128	DB	CCCTTTGTGTACATCGTGTCTGTGAGAGCTTCCGCAACCGTTGGTCTCTGCGGTGA	1187
966	QY	AAGAGCGACTGGAAGGAAATCAACAAATATGGGAAACACTCTGA	1009
1188	DB	GCCTGACGCCCGGGCAGCTTCGCGTGTGCAGCAACGCTCAGA	1231

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RESULT 11
US-09-478-601-1
; Sequence 1, Application US/09478601
; Patent No. 6221616
; GENERAL INFORMATION:
; APPLICANT: Salen, John A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Negorrry, Raissa
; APPLICANT: Wilson, Amy B.
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
; TITLE OF INVENTION: Receptor (NCHI) And Uses Thereof
; FILE REFERENCE: 574532\JFW
; CURRENT APPLICATION NUMBER: US/09/478,601
; CURRENT FILING DATE: 2000-01-06
; EARLIER APPLICATION NUMBER: 09/224,426
; EARLIER FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 1
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-478-601-1

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RESULT 12  
US-09-478-602-1  
; Sequence 1, Application US/09478602  
; Patent No. 6291195  
; GENERAL INFORMATION:  
; APPLICANT: Salom, John A.  
; APPLICANT: Laz, Thomas M.  
; APPLICANT: Nagorny, Raisa  
; APPLICANT: Wilson, Amy E.  
; TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone  
; TITLE OF INVENTION: Receptor (MCH1) And Uses Thereof  
; FILE REFERENCE: 57453yJPW  
; CURRENT APPLICATION NUMBER: US/09/478,602  
; CURRENT FILING DATE: 2000-01-06  
; EARLIER APPLICATION NUMBER: 09/224,426  
; EARLIER FILING DATE: 1998-12-31  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1269  
; TYPE: DNA  
; ORGANISM: Homo sapiens



US-09-478-602-1

Query Match 12.7%; Score 130.4; DB 3; Length 1269;  
Best Local Similarity 50.1%; Pred. No. 1.1e-31;  
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;

186 CAGGAAAAAACAAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245  
Db |||||  
423 CTGGTGCACAAAGCTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTCTT 482  
Qy |||||  
246 CATAGTTGGAATGCTTTTCTTATTCACCAATGGGCGGAGGGGAGAGTGGTGTGG 305  
Db |||||  
483 TCTCTGGGATGCTTCTATGATTCACCAAGCTCATGGGCAATGGGGTGTGGCACTTTGG 542  
Qy |||||  
306 GGGGCTCTCTGACCATCATCATCCCTGGATCTGTGAACCAATTTGCCCTGTAGTGC 365  
Db |||||  
543 GGAGACCATGTGACCCCTCATACGGCCATGGATGCCAATAGTCAGTTCCACGACCTA 602  
Qy |||||  
366 CATCATGACTGTAATGAGTGTGACAGGTAATTTGGCCCTGTCCCAACCAATTTGAGTAC 425  
Db |||||  
603 CATCTGACCGCATGCCATGACCGTACTCTGGCCACTGTCCACCCCATCTCTTCCAC 662  
Qy |||||  
426 ACCTTGAGACACAGGTACAGACCATCCGATCAATTTGGGCTTTGGGCACTTCTCT 485  
Db |||||  
663 GAAGTTCGGAAGCCCTCTGTGCGCCACCTGGTGTGCTCTCTGTGGCCCTCTCTCT 722  
Qy |||||  
486 TATCTGGCATTTGCTCTGGGTCTACTCGAAGGTCTCAAAATTTAAAGACGGTGTGA 545  
Db |||||  
723 CATCAGCATCACCCCTGTGTGGCTGTATGCGACACTATCCCTTCCAGGAGTGCAGT 782  
Qy |||||  
546 GAGTTGTCTTTGATTTGATGATCCCTGACAGTGTACTCTGTGTATACACTTTATTTGAC 605  
Db |||||  
783 GGGCTGCGGATACGCTGCGCCAAACCCAGACACTGACCTCT-----ACTGGTTTACC 834  
Qy |||||  
606 GATTAACAACTTTTTTTTCCCTCTACCCCTGATTTGGTGTGTATATTTAAATTTATG 665  
Db |||||  
835 CTGTACACAGTTTTTCTGGGCTTTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 894  
Qy |||||  
666 CTATCTGAGGATGATPATCAACAGATAAGGATGCGAGATGCTGAATCCAGTGTAC 725  
Db |||||  
895 AGGATCTGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 950  
Qy |||||  
726 AAGACAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1007  
Db |||||  
951 GCTGCGGACA---AAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1067  
Qy |||||  
786 GAGTGTGCTGCTTATCATGTGATCAAACTGGTGAACCTTACAGATGGAACAGCCCACT 845  
Db |||||  
1008 GTGCTGGGACCCCTACTATGTGTACAGCTGACCCAGTTGTCCATCAGCGCCGACCT 1067  
Qy |||||  
846 GGCCTTCTATGTTGTTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 905  
Db |||||  
1068 CACCTTTGTCTACTATACAAATGCGGCAATCAGCTTGGGCTATGCAACAGCTGTCTCA 1127  
Qy |||||  
906 CCCTTTTCTCTACATCTGCTGATGGAATTTCCAGAAACGCTCTGCTCAAAATCCAAAG 965  
Db |||||  
1128 CCCCCTTGTGTATGATGCTCTGTGAGAGTTCCGCAACGCTTGGTCTCTGTGTGTGA 1187  
Qy |||||  
966 AAGAGGACTGTAGAAGAAATCAACAAATATGGAAACACTCTGA 1009  
Db |||||  
1188 GCCTGACGCCCGGCGAGCTTCCGCTGTGAGCAACGCTCTGA 1231

RESULT 13

US-08-602-809-1  
; Sequence 1, Application US/08602809  
; Patent No. 6008012  
; GENERAL INFORMATION:  
; APPLICANT: BERGMA, DERK  
; APPLICANT: ELLIS, CATHERINE  
; TITLE OF INVENTION: HUMAN SOMATOSTATIN-LIKE R  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 3

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia  
STREET: P.O. Box 980  
CITY: Valley Forge  
STATE: PA  
COUNTRY: US  
ZIP: 19482-0980  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,809  
FILING DATE: 13-JUN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/16472  
FILING DATE: 15-DEC-1995  
APPLICATION NUMBER: US 08/357,675  
FILING DATE: 16-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Prestia, Paul F  
REGISTRATION NUMBER: 23,031  
REFERENCE/DOCKET NUMBER: PS0277  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 601-407-0700  
TELEFAX: 610-407-0701  
TELEX: 846169  
INFORMATION FOR SEQ ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1316 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-602-809-1

Query Match 12.7%; Score 130.4; DB 3; Length 1316;  
Best Local Similarity 50.1%; Pred. No. 1.2e-31;  
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;

Qy 186 CAGGAAAAAACAAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245  
Db 389 CTGGTGCACAAAGCTCCCGACATCTTCATCATCAACCTCTCGTAGTAGATCTCTCTT 448  
Qy 246 CATAGTTGGAATGCTTTTCTTATTCACCAATGGGCGGAGGGGAGTGGTGTGG 305  
Db 449 TCTCTGGGATGCTTCTATGATTCACCAAGCTCATGGGCAATGGGCTGTGGCACTTTGG 508  
Qy 306 GGGGCTCTCTGACCATCATCATCCCTGGATCTGTAAACCAATTTCCCTGTAGTGC 365  
Db 509 GGAGACCATGTGACCCCTCATCAGGCCATGGATGCCAATAGTCAGTTCACGACCTA 568  
Qy 366 CATCATGACTGTAATGAGTGTGGAAGTACTTTGCCCTCGTCCAAACCAATTTGCACTGAC 425  
Db 569 CATCTGACCGCCATGGCCATTTGACCGCTACTCGCCACTGTCCACCCCATCTCTTCCAC 628  
Qy 426 ACCTTGAGAACAGGTACAGACCATCCGATCAATTTGGGCTTTGGGCACTTCTCTT 485  
Db 629 GAAGTTCGGAAGCCCTCTGTGGCCACCCCTGTGATCTGCTCTGTGGGCTCTCTCTT 688  
Qy 486 TATCTGGCATTTGCTGTGGGTCTACTCGAAGGTCTCAAAATTTAAAGACGGTGTGA 545  
Db 689 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTATCCCTTCCAGGAGTGCAGT 748  
Qy 546 GAGTTGTCTTTGATTTGATGATCCCTGAGGATGACTCTGTGTATACACTTTATTTGAC 605  
Db 749 GGGCTGCGGATACGCTGCGCAACCCAGACACTGACCTCT-----ACTGGTTTACC 800  
Qy 606 GATTAACAACTTTTTTTTCCCTCTACCCCTGATTTGGTGTGTATATTTAAATTTATG 665  
Db 801 CTGTACCAAGTTTTTCTGGGCTTTGGCTTGTGCTGTGCTATCATCAGCGGATAGTGT 860



QY 666 CTATCTTGGGAGATGATATCAACAGAAATAGGATCCAGAGCTGCAATCCAGTGTACC 725  
Db 861 AGGATCCTCAGCGATGACGCTCTCA-----GTGGCCCCCGCTCCAGCGCAGCATCG 916  
QY 725 AAAACAGAGAGTGAAGTTCACAAAGATGCTGTGCTGTGCTGTGCTGTGCTGTGCT 785  
Db 917 GCTGGGACA---AAGAGGTGACCGGCACAGCATGCGCATCTCTGCTGCTCTTTTGT 973  
QY 786 GAGTGTGCTGCTTATCATGTGATACAACTGGTGAACCTTACAGATGGAACAGCCACACT 845  
Db 974 GTGTGGGACCCCTACTATGTCTACAGCTGACCCAGTTGTCATCAGCGCCCGACCT 1033  
QY 846 GGCCTTCTATGCTGTTATCTCTCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905  
Db 1034 CACCTTTGTCTATTATCAATGCGGCCATCAGCTTGGGCTATGCCAAGCTGCTCAA 1093  
QY 906 CCGCTTTCTCTACCTCTGCTGAGTGAATTTCCAGAAACCTGCTGCTCAATCCAAAG 965  
Db 1094 CCGCTTTGTCTATCTGCTCTGTGAGAGCTTCCGCAACGCTGGTCTGCTGCTGCT 1153  
QY 966 AAGAGGATGAGAGGAATCAACAAATATGGGAACACTCTGA 1009  
Db 1154 GCGTGCAGCCAGGCGAGCTTGGGCTGTGCAACGCTCAGA 1197

RESULT 14  
PCT-US95-16472-1  
; Sequence 1, Application PC/TUS9516472  
; GENERAL INFORMATION:  
; APPLICANT: Bergsma, Derk J  
; APPLICANT: Ellis, Catherine E  
; TITLE OF INVENTION: Human Somatostatin Receptor  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation/Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P. O. Box 1539-UM2220  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/16472  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50277  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270 5024  
; TELEFAX: 610 270 5090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1316 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 27..1232  
; OTHER INFORMATION: /note= "The coding sequence is from  
; OTHER INFORMATION: nucleotides 27 to 1232."  
PCT-US95-16472-1

Query Match 12.7%; Score 130.4; DB 5; Length 1316;

Best Local Similarity 50.1%; Pred. No. 1.2e-31;  
Matches 413; Conservative 0; Mismatches 396; Indels 15; Gaps 3;  
QY 186 CAGAAAAAACAAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTGATTTGGTCCA 245  
Db 389 CTGGTGCACAACAGTCCCGACATCTTCAATCACTCACTCTCGGTAGTAGATCTCTCTTT 448  
QY 246 CATAGTTGGATGCTTTTCTTATTACCAATGGGCGGAGGAGAGTGGTGGTGGTGG 305  
Db 449 TCTCCTGGGATGCGCTTTCATGATCCACAGCTCATGGGCAATGGGGTGTGGCACTTTGG 508  
QY 306 GGGGCTCTCTGCAACCATCATCATCCCTGGATCTTTGTAACCAATTTCCCTGTAGTGC 365  
Db 509 GGAGACCATGTGCACCTCATCAGGCCATGATGCAATAGTCAGTTTCCACAGCCTA 568  
QY 366 CATCATGACTGTATAGTGTGGACAGTACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425  
Db 569 CATCCTGACCGCATGCGCTTACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 628  
QY 426 AGTTGGAGAACAAAGGTACAAGACCATCCGATCAATTTGGGCTTTGGGCGAGCTTCTCT 485  
Db 629 GAAGTTCCGAGGCCCTCTGTGGCCACCTGGTGAATGCTGCTCTGTGGGCGCTCTCT 688  
QY 486 TATCCTGGCATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545  
Db 689 CATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCTTCCACAGAGTGCAGT 748  
QY 546 GAGTTGTGCTTTGATTTGATATCCCTGAGTGTACTCTGCTGCTGCTGCTGCTGCTGCT 605  
Db 749 GGGCTGCGGCATACGCTGCGCCAAACCCAGACACTGACCTCT-----ACTGCTTCA 800  
QY 606 GATAACAACTTTTTCCTCTTACCCCTTGAATTTTGGTGTGCTGCTGCTGCTGCTGCT 665  
Db 801 CTGTACCAAGTTTTCCTGGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860  
QY 666 CTATCTGGGAGATGATATCAACAGATAGGATGCGAGATGCTGCAATCCAGTGTACC 725  
Db 861 AGGATCCTGCGAGCATGAGTCTCTCA-----GTGGCCCCCGCTCCAGCGCAGCATCCG 916  
QY 726 AAAACAGAGAGTGAATGAAATGCAAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 785  
Db 917 GCTGCGGACA---AAGAGGTGACCCCGCAGCCATCGCCATCTGCTGCTGCTTGTGT 973  
QY 786 GAGTGTGCTGCTTATCATGTGATACAACTGGTGAATTTACAGATGGAACAGCCACACT 845  
Db 974 GTGCTGGGCAACCTTACTATGCTGTACAGCTGACCCAGTTGCTCCATCAGCGCCCGAC 1033  
QY 846 GGCCTTCTATGCTGGTATTACCTCTCCATCTGCTCAGCTATGCCAGCAGCAGCATTA 905  
Db 1034 CACCTTTGTCTATTATACAAATGCGGCCATCAGCTTGGGCTATGCCAAGCTGCTCAA 1093  
QY 906 CCGCTTTCTCTACATCCTGCTGATGGAATTTCCAGAAACGCTGTGCTCAATCCAAAG 965  
Db 1094 CCGCTTTGTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1153  
QY 966 AAGAGCAGCTGAGAGGAATCAACAAATATGGGAACACTCTGA 1009  
Db 1154 GCGTGCAGCCAGGCGAGCTTGGGCTGTGCAACGCTCAGA 1197

RESULT 15  
US-08-984-288-1  
; Sequence 1, Application US/08984288  
; Patent No. 6033872  
; GENERAL INFORMATION:  
; APPLICANT: BERGSM, DEREK  
; APPLICANT: ELLIS, CATHERINE  
; TITLE OF INVENTION: NOVEL HUMAN 11CB SPLICE V  
; TITLE OF INVENTION: ASIAN  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: RATNER & PRESTIA  
; STREET: P.O. BOX 980



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 17, 2004, 16:04:17 ; Search time 3085 Seconds  
(without alignments)  
9902.435 Million cell updates/sec

Title: US-09-913-770B-2

Perfect score: 1023

Sequence: 1 atgaatccatttcagcatc.....ctctgaatcacacttttag 1023

Scoring table: IDENTITY NUC

Gapop 10.0 , Capext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: em\_estov:\*\*

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7: em\_estro:\*\*

8: em\_htc:\*\*

9: gb\_est1:\*\*

10: gb\_est2:\*\*

11: gb\_htc:\*\*

12: gb\_est3:\*\*

13: gb\_est4:\*\*

14: gb\_est5:\*\*

15: em\_estfun:\*\*

16: em\_estom:\*\*

17: em\_gss\_hum:\*\*

18: em\_gss\_inv:\*\*

19: em\_gss\_pln:\*\*

20: em\_gss\_vrt:\*\*

21: em\_gss\_fun:\*\*

22: em\_gss\_mam:\*\*

23: em\_gss\_mus:\*\*

24: em\_gss\_pro:\*\*

25: em\_gss\_rod:\*\*

26: em\_gss\_pbg:\*\*

27: em\_gss\_vrl:\*\*

28: gb\_gss1:\*\*

29: gb\_gss2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	590	57.7	2372	11 BCO38441	BCO38441 Homo sapi
3	515.8	50.4	960	12 B1914562	B1914562 603179505
4	438	42.8	507	13 BX279838	BX279838 BX279838

C	5	215.4	21.1	925	28	AQ747249	AQ747249 HS_5537 A
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C	8	195.4	19.1	519	28	AQ190629	AQ190629 HS_3226 A
C	9	182.4	17.8	879	13	BQ953496	BQ953496 AGENCOURT
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C	11	125	12.2	764	14	CF147818	CF147818 AGENCOURT
C	12	120.2	11.7	429	28	AQ492353	AQ492353 HS_5123 A
C	13	106.6	10.4	723	14	CF147812	CF147812 AGENCOURT
C	14	106.6	10.4	988	13	EX346496	EX346496 BX346496
C	15	106.6	10.4	1012	13	EX367456	EX367456 BX367456
C	16	105	10.3	872	12	BI757659	BI757659 603027991
C	17	100.8	9.9	958	12	BI754621	BI754621 603025173
C	18	97	9.5	1114	12	EM805549	EM805549 AGENCOURT
C	19	96.8	9.5	912	13	EX326588	EX326588 BX326588
C	20	94.6	9.2	955	13	EX374433	EX374433 BX374433
C	21	89.6	8.8	797	12	BI818742	BI818742 603037572
C	22	89.4	8.7	996	13	EX350008	EX350008 BX350008
C	23	88.8	8.7	921	12	BG913631	BG913631 602811509
C	24	87.2	8.5	707	13	BY724157	BY724157 BX724157
C	25	86.2	8.4	537	9	AL921401	AL921401 AL921401
C	26	83.8	8.2	1101	13	EX403473	EX403473 BX403473
C	27	83.2	8.1	903	14	CD252714	CD252714 AGENCOURT
C	28	83	8.1	1053	28	CC187882	CC187882 CH261-808
C	29	82.2	8.0	2405	11	AK038389	AK038389 Mus muscu
C	30	81.4	8.0	681	29	BX149173	BX149173 Danio rer
C	31	80.8	7.9	345	14	F07228	F07228 HSC1ZF101 n
C	32	80.8	7.9	513	14	CB054665	CB054665 NISC_gm05
C	33	79	7.7	1006	29	AY400674	AY400674 Homo sapi
C	34	78.6	7.7	1257	29	AY400332	AY400332 Homo sapi
C	35	77.8	7.6	1088	13	EX403468	EX403468 BX403468
C	36	77.6	7.6	468	13	BX281894	BX281894 BX281894
C	37	77.4	7.6	1257	29	AY400333	AY400333 Pan trogl
C	38	77	7.5	730	14	CF147825	CF147825 AGENCOURT
C	39	76.6	7.5	642	10	BE252309	BE252309 60114162
C	40	76.6	7.5	729	14	CF147826	CF147826 AGENCOURT
C	41	76.6	7.5	768	14	CF996790	CF996790 AGENCOURT
C	42	76.6	7.5	821	14	CK239769	CK239769 AGENCOURT
C	43	72.4	7.1	904	12	BG329444	BG329444 602429002
C	44	72.4	7.1	1006	29	AY400676	AY400676 Mus muscu
C	45	72.4	7.1	1089	29	AY400988	AY400988 Mus muscu

#### ALIGNMENTS

RESULT 1  
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LOCUS AGENCOURT\_14740196 NIH MGC\_145 Homo sapiens cDNA clone  
DEFINITION IMAGE:6971912 5', mRNA sequence.  
ACCESSION CF147811  
VERSION CF147811.1 GI:33244079  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 730)  
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [csapbs-remail.nih.gov](mailto:csapbs-remail.nih.gov)  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov  
Plate: IRB102 row: c column: 07  
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Location/Qualifiers  
1. 730  
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/mol\_type="mRNA"  
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/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_145"  
/notes="vector: pCDNA3.1; site\_1: varies by clone; site\_2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmiI/XhoI-3', 5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearranged\_plates/IRB1\_presv.dat  
a Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 68.4%; Score 699.8; DB 14; Length 730;  
Best Local Similarity 99.7%; Pred. No. 6.9e-164;  
Matches 701; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAATCCATTTCATGCATCTTGTGGAAACACCTCTGCGGAATTTTAAACAAATCCTGG 60  
DB 28 ATGAATCCATTTCATGCATCTTGTGGAAACACCTCTGCGGAATTTTAAACAAATCCTGG 87  
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DB 88 AATTAAGAGTTGCTTATCAAACTGCAGTGTGTAGATACATCTCTCCCTCCATG 147  
QY 121 ATTGGGATATCTGTTCAACAGGCTGTTTGGCAACATCTCTATTTTACTATAATA 180  
DB 148 ATTGGGATATCTGTTCAACAGGCTGTTTGGCAACATCTCTATTTTACTATAATA 207  
QY 181 AGATCCAGGAAAAAAGTCCCTGACATCTATCTGCAACCTGCTGTGCTGATTTG 240  
DB 208 AGATCCAGGAAAAAAGTCCCTGACATCTATCTGCAACCTGCTGTGCTGATTTG 267  
QY 241 GTCCACATAGTTGAATGCTTTTCTTATTCACATGGCCCGAGGGAGAGTGGGTG 300  
DB 268 GTCCACATAGTTGAATGCTTTTCTTATTCACATGGCCCGAGGGAGAGTGGGTG 327  
QY 301 TTTGGGGGGCTCTCTGCACATCATCATCTCTGATCTGTAAACCAATTTGCTGT 360  
DB 328 TTTGGGGGGCTCTCTGCACATCATCATCTCTGATCTGTAAACCAATTTGCTGT 387  
QY 361 AGTCCATCATGCTGAATGAGTGGAGAGTACTTTGCCCTCGTCCAAACCATTTCA 420  
DB 388 AGTCCATCATGCTGAATGAGTGGAGAGTACTTTGCCCTCGTCCAAACCATTTCA 447  
QY 421 CTGACAGCTTTGGAGAACAGGTACAAGACCATCCGATCAATTTGGGCCCTTTGGG 480  
DB 448 CTGACAGCTTTGGAGAACAGGTACAAGACCATCCGATCAATTTGGGCCCTTTGGG 507  
QY 481 TCCTTTATCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
DB 508 TCCTTTATCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 557  
QY 541 GTTGAGAGTTGTGCTTTTGTATTTGACATCCCTGACATGCTACTCTGTTATACATTTAT 600  
DB 568 GTTGAGAGTTGTGCTTTTGTATTTGACATCCCTGACATGCTACTCTGTTATACATTTAT 627  
QY 601 TTGACGATACAACTTTTTCCTCTACCTTGTATTTTGGTGTGCTATTTTAAAT 660  
DB 628 TTGACGATACAACTTTTTCCTCTACCTTGTATTTTGGTGTGCTATTTTAAAT 687  
QY 661 TTATGCTATATCTGGGAGATGTATCAACAGATGATGCA 703

688 TTATGCTATATCTGGGAGATGTTATTCACAGATAGGATGCCA 730

DB  
RESULT 2  
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LOCUS  
DEFINITION  
ACCESSION  
BC038441  
VERSION  
BC038441.1  
KEYWORDS  
GI:23620386  
SOURCE  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2372)  
Direct Submission  
Strausberg, R.  
Submitted (04-OCT-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc.mgc@hgrl.nih.gov  
Ahter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, J., Gupta, J., Hegnighi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maduro, Q.I., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
Tougeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, B.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAP Plate: 62 Row: n Column: 20  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 14210483  
This clone has the following problem: retained intron.

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/clone="IMAGE:5243616"  
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/lab\_host="DH10B"  
/note="vector: pCMV-SPORT6"

ORIGIN  
Query Match 57.7%; Score 590; DB 11; Length 2372;  
Best Local Similarity 100.0%; Pred. No. 2.1e-136;  
Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATCCATTTCATGCATCTTGTGGAAACACCTCTGCGGAATTTTAAACAAATCCTGG 60  
DB 70 ATGAATCCATTTCATGCATCTTGTGGAAACACCTCTGCGGAATTTTAAACAAATCCTGG 129  
QY 61 AATTAAGAGTTGCTTATCAAACTGCAGTGTGTAGATACATCTCTCCCTCCATG 120  
DB 130 AATTAAGAGTTGCTTATCAAACTGCAGTGTGTAGATACATCTCTCCCTCCATG 189  
QY 121 ATTGGGATATCTGTTCAACAGGCTGTTGGCAACATCTCTCAATTTGTTACTATAATA 190



Hurban Unigeneset - RZPD3 (RZPDLIB No. 972)  
 http://www.rzpd.de/CloneCards/Cgi-  
 bin/showfile.pl.cgi?response?libNo=972  
 RZPD Deutsches Ressourcenzentrum fuer  
 Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel. +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD; contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer: M13u. Primer sequence: CGTTGTAAACGACGCCAGT.

## FEATURES

source

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1. 507
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/db_xref="taxon:9606"
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e-98;
Matches 438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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121	ATTGGGATTATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTTGTAATTCATAATA	180
190	ATTGGGATTATCTGTTCAACAGGCTGGTTGGCAACATCCTCATTTGTAATTCATAATA	249
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250	AGATCCAGGAAAAAACAAGTCCCTGACATCTATATCTGCAACTGTGGCTGATTGG	309
241	GTCCACATAGTTGGAATGCCCTTTTCTTATTACCAATGGCCCGAGGGAGAGTGGGTG	300
310	GTCCACATAGTTGGAATGCCCTTTTCTTATTACCAATGGCCCGAGGGAGAGTGGGTG	369
301	TTTGGGGGCTCTCTGCACCATCATCATCCCTGGATACTTGTAAACCAATTTGCCCTG	360
370	TTTGGGGGCTCTCTGCACCATCATCATCCCTGGATACTTGTAAACCAATTTGCCCTG	429
361	AGTGGCATCATGACTGTAACTCAGTGTGGACAGGTACTTTGCCCTCGTCCAAACCATTTGCA	420
430	AGTGGCATCATGACTGTAACTCAGTGTGGACAGGTACTTTGCCCTCGTCCAAACCATTTGCA	489
421	CTGACACGTTGGAGAACA	438
490	CTGACACGTTGGAGAACA	507

[illegible]

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

## REFERENCE AUTHORS

TITI, R.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

10445704  
Contact: Mahiraj GG, Wallace JC, Hood L.

Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887

Email: [wallace@u.washington.edu](mailto:wallace@u.washington.edu)  
 Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong ([pieter@dong.med.buffalo.edu](mailto:pieter@dong.med.buffalo.edu)). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>) or from Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end Web Server: <http://www.htsc.washington.edu>  
 plate: 1113 row: G column: 17

Seq primer: 17  
Class: BAC ends

Class: bac emb  
High quality sentence stop: 925.

## FEATURES

SPILLAGE

1. 925

ATTENTION /

Т. 1. - С. 262. "Отечественная война 1812 года"

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РД "Машин" /

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Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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534 TCAGATCCAGGAAAAAACAGTCCCTGACATCTATATCTGCAACCTGGCTGCTGGCTGAT 473

298

QY  
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474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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DEFINITION	RPC111-100N2.TV	RPC1-11	Homo sapiens	genomic clone	RPC1-11-100N2,

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genomic survey sequence.
ACCESSION AQ311725
VERSION AQ311725.1 GI:4043474
KEYWORDS CSS.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of human BAC end sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@igr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.5e-39;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 390 CAGGTACTTTGCCCTCGTCCACCATTTTCGACTGACACGTTGGAGACAGGTACAAGAC 449
Db 367 CAGGTACTTTGCCCTCGTCCACCATTTTCGACTGACACGTTGGAGACAGGTACAAGAC 308
QY 450 CATCCGGATCAATTTGGGCGCTTTGGCAGCTTCCTTTATCCTGGCATTGCCGTCTGGGT 509
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QY 510 CTACTCGAAGTCAATCAAAATTTAAAGACGGTGTGAGAGTTGCTTTGATTGACATC 569
Db 247 CTACTCGAAGTCAATCAAAATTTAAAGACGGTGTGAGAGTTGCTTTGATTGACATC 188
QY 570 CCTGACGATGTACTCTGGTA 590
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LOCUS AGI18972 714 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-127E10.R, genomic survey sequence.
ACCESSION AGI18972
VERSION AGI18972.1 GI:16739491
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

genomic survey sequence.
ACCESSION AQ311725
VERSION AQ311725.1 GI:4043474
KEYWORDS CSS.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of human BAC end sequences for Sequence-Ready Map Building
JOURNAL Unpublished (1998)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@igr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html
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                     RPCI11 Human Male BAC Library"
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Query Match      19.6%; Score 201; DB 28; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.5e-39;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 390 CAGGTACTTTGCCCTCGTCCACCATTTTCGACTGACACGTTGGAGACAGGTACAAGAC 449
Db 367 CAGGTACTTTGCCCTCGTCCACCATTTTCGACTGACACGTTGGAGACAGGTACAAGAC 308
QY 450 CATCCGGATCAATTTGGGCGCTTTGGCAGCTTCCTTTATCCTGGCATTGCCGTCTGGGT 509
Db 307 CATCCGGATCAATTTGGGCGCTTTGGCAGCTTCCTTTATCCTGGCATTGCCGTCTGGGT 248
QY 510 CTACTCGAAGTCAATCAAAATTTAAAGACGGTGTGAGAGTTGCTTTGATTGACATC 569
Db 247 CTACTCGAAGTCAATCAAAATTTAAAGACGGTGTGAGAGTTGCTTTGATTGACATC 188
QY 570 CCTGACGATGTACTCTGGTA 590
Db 187 CCTGACGATGTACTCTGGTA 167

RESULT 7
AGI18972
LOCUS AGI18972 714 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-127E10.R, genomic survey sequence.
ACCESSION AGI18972
VERSION AGI18972.1 GI:16739491
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 714)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimps@gsr.riken.go.jp; URL:http://hgp.gsc.riken.go.jp/;
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
     source           1..714
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-127E10.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
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Query Match      19.2%; Score 196.8; DB 29; Length 714;
Best Local Similarity 99.0%; Pred. No. 2.9e-38;
Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 390 CAGGTACTTTGCCCTCGTCCACCATTTTCGACTGACACGTTGGAGACAGGTACAAGAC 449
Db 141 CAGGTACTTTGCCCTCGTCCACCATTTTCGACTGACACGTTGGAGACAGGTACAAGAC 200
QY 450 CATCCGGATCAATTTGGGCGCTTTGGCAGCTTCCTTTATCCTGGCATTGCCGTCTGGGT 509
Db 201 CATCCAGATCAATTTGGGCGCTTTGGCAGCTTCCTTTATCCTGGCATTGCCGTCTGGGT 260
QY 510 CTACTCGAAGTCAATCAAAATTTAAAGACGGTGTGAGAGTTGCTTTGATTGACATC 569
Db 261 CTACTCGAAGTCAATCAAAATTTAAAGACGGTGTGAGAGTTGCTTTGATTGACATC 320
QY 570 CCCTGACGATGTACTCTGGT 589
Db 321 CCCTGACGATGTACTCTGGT 340

RESULT 8
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LOCUS AQ190629 519 bp DNA linear GSS 04-NOV-1998
DEFINITION HS 3226_A1_H07_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3226 Col=13 Row=O, genomic survey
sequence.
ACCESSION AQ190629
VERSION AQ190629.1 GI:3589551
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 519)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

```

**TITLE** Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
**MEDLINE** 93380589  
**PUBMED** 10449764  
**COMMENT** Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 3226 row: O column: 13  
 Class: BAC ends  
 High quality sequence stop: 519.

**FEATURES**  
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 1..519  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=3226 Col=13 Row=O"  
 /sex="male"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /notes="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

**ORIGIN**  
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 Best Local Similarity 97.1%; Pred. No. 6.2e-38;  
 Matches 199; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 386 TGCACAGTACTTGCCTCGCTCCACCACTTCGATCGACCTTCGAGACCAAGTACA 445  
 Db 419 TGTGACGATCTTGTGCTTCGTCACCACTTCGATCGACCTTCGAGACCAAGTACA 360  
 QY 446 AGACCACTCGGATCAATTTGGGCTTTGGGAGCTTCCTTTATPCCTGGCATTCCTGTCT 505  
 Db 359 AGACCACTCGGATCAATTTGGGCTTTGGGAGCTTCCTTTATPCCTGGCATTCCTGTCT 300  
 QY 506 GGGTCTACTCGAGGTCATCAAAATTTAAGACCGTGTGAGATTTGCTTTGATTTGA 565  
 Db 299 GGGTCTACTCGAGGTCATCAAAATTTAAGACCGTGTGAGATTTGCTTTGATTTGA 240  
 QY 566 CATCCCTCGAGTACTCTGCTA 590  
 Db 239 CATCCCTCGAGTACTCTGCTA 215

**RESULT 9**  
 BQ953496/c  
**LOCUS** BQ953496 879 bp mRNA linear EST 21-AUG-2002  
**DEFINITION** AGENCOURT 8841637 Lupski sciatic\_nerve Homo sapiens cDNA clone  
 IMAGE:6193194 5', mRNA sequence.  
**ACCESSION** BQ953496  
**VERSION** BQ953496.1 GI:22368974  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 879)  
**REFERENCE** NIH-MGC http://mgi.nci.nih.gov/  
**AUTHORS** National Institutes of Health, Mammalian Gene Collection (MGC)  
**TITLE** Unpublished (1999)  
**JOURNAL** Contact: Robert Strausberg, Ph.D.  
**COMMENT** Email: coapbs-x@mail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
 Plate: LHAM13612 row: a column: 19  
 High quality sequence stop: 612.  
**FEATURES**  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:6193194"  
 /sex="male"  
 /tissue\_type="sciatic nerve"  
 /dev stage="adult, 70 yr"  
 /lab host="DH10B"  
 /clone\_lib="Lupski sciatic nerve"  
 /note="Vector: PMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACGCTCCG-3' and  
 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >  
 1 kb for average insert length 1.87 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

**ORIGIN**  
 Query Match 17.8%; Score 182.4; DB 13; Length 879;  
 Best Local Similarity 99.5%; Pred. No. 1.2e-34;  
 Matches 183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATCCATTTCATGATCTTGTGGAACACCTCTCCGAACTTTTAAACAATCTCG 60  
 Db 501 ATGAATCCATTTCATGATCTTGTGGAACACCTCTCCGAACTTTTAAACAATCTCG 442  
 QY 61 AATAAGAGTTTGTCTTATCAACCTGCTGTAGATACAGTCATCTCCCTCCATG 120  
 Db 441 AATAAGAGTTTGTCTTATCAACCTGCTGTAGATACAGTCATCTCCCTCCATG 382  
 QY 121 ATTGGGATTTCTTTCAACAGGCTGTTGGCAACATCTCTCATTTATCAATAA 180  
 Db 381 ATTGGGATTTCTTTCAACAGGCTGTTGGCAACATCTCTCATTTATCAATAA 322  
 QY 181 AGAT 184  
 Db 321 AGGT 318

**RESULT 10**  
 CES16999/c  
**LOCUS** CES16999 653 bp DNA linear GSS 28-SEP-2003  
**DEFINITION** tigr-gss-dog-1700327417623 Dog Library Canis familiaris genomic,  
 genomic survey sequence.  
**ACCESSION** CES16999  
**VERSION** CES16999.1 GI:36833780  
**KEYWORDS** GSS.  
**SOURCE** Canis familiaris (dog)  
**ORGANISM** Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 653)  
**REFERENCE** Kirkness E.F., Bafna V., Halpern A.L., Levy S., Remington K.,  
 Rusch D.B., Delcher A.L., Pop M., Wang W., Fraser C.M. and  
 Venter J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
**JOURNAL** MEDLINE 22875432  
**PUBMED** 14512627  
**COMMENT** Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208



```

Email: ekirknes@tigr.org
Class: shotgun.
       Location/Qualifiers
       1..653
       /organism="Canis familiaris"
       /mol_type="genomic DNA"
       /strain="Standard Poodle"
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       /note="Site 1: Batxi; Libraries were prepared from
peripheral blood"
FEATURES
             source

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## ORIGIN

Query Match	14.2%	Score 145.6;	DB 29;	Length 653;
Best Local Similarity	87.0%;	Pred. No. 1.7e-25;		
Matches 160;	Conservative 0;	Mismatches 24;	Indels 0;	Gaps 0;

  

QY	1	ATGAATCCATTTCATGCAATCTTGTTGGAACACCTCTGCGAACCTTTTAAACAAATCTCTGG	60
Db	253	ATGTAATCACTTCACTCATCTCTGTTGGAACACCTCTGCTGAACCTTTGAAACAAATCTCTGC	194
QY	61	AATAAAGAGTTTGCTTATCAAACTGCCAGTGTGGTAGATACAGTCATCCTCCCTTCCTCATG	120
Db	193	AATAAAGAGTTTGCTTATCAACCCCTCAGCATTTTAGATACAATCATCTCCCTCTCTATG	134
QY	121	ATTGGGATATCTGTTTCAACAGGCTGGTTGGCAACATCCTCATTTGATTCACTATAATA	180
Db	133	ATTGGGATATCTGTTTCAATGGGGCTAGTTGGCAACATCCTCATTTGATTCACTATAATA	74
QY	181	AGAT 184	
Db	73	AGGT 70	

## RESULT 11

CF147818	764 bp	mRNA	linear	EST 25-JUL-2003
LOCUS				
DEFINITION	AGENCOURT 14740235 NIH MGC_145 Homo sapiens cDNA clone IMAGE:6571905 5', mRNA_sequence.			
ACCESSION	CF147818			
VERSION	CF147818.1			
KEYWORDS	GI:33244086			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 764)			
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Daniela S. Gerhard Ph.D.			

COMMENT

Office of Cancer Genomics  
National Cancer Institute / NTH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabs-@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.linl.gov>  
Plate: IRS102 row: b column: 12  
High quality sequence start: 11  
High quality sequence stop: 765.

## FEATURES

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/mol_type="mRNA"
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/clone_lib="NIH_MGC_145"
/notes=vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (RA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearview_plates/IR91.presv.dat
A note: this is a NIH MGC Library."
```

## ORIGIN

Query Match	12.2%; Score 125; DB 14; Length 764;
Best Local Similarity	55.2%; Pred. No. 2.5e-20;
Matches	273; Conservative 0; Mismatches 20; Indels 12; Gaps 1;
QY	104 TCATCTCCCTTCATGATGGATATATCTGTTCAACAGGCTGGTTGGCAACATCCTCA 163
Db	163 TCATTATGCTTCCGTGTTGGTACCATCTGCTCTCTGGGCATCTGTGGGAAATCCACGG 222
QY	164 TTGTATTTCATAATAA-----GATCCAGGAAAAAACAAGTCCCTGCACATCT 211
Db	223 TCATCTTTGTGGTGAAGACTCCAAGTACACTGTTGCAGCAACGTCCTCGACATCT 282
QY	212 ATATCTGCAACCTGGCTGTGGCTGATTGGTGCACATAGTTGGAATGCCTTTTCTATTTC 271
Db	283 TCATCATCAACCTCTCTGTGGTAGATCTGCTTCTCTGCTGGGCATGCGCTTTTCATGATCC 342
QY	272 ACCAATGGCCGAGGGGAGAGTGGTGTTTGGGGGCGCTCTCTGCACCATCATCACAT 331
Db	343 ACCAGCTATGGGGAAACGGCGTCTGGCACTTTTGGGGAACCAATGTGCACCTCATCACAG 402
QY	332 CCCTGGATACCTTTGAACCAATTGCTGTAGTGCCATCATGACTGTAATGAGTGTGGACA 391
Db	403 CCATGAGCCCAACAGTCACTGTTCACTAGCACCTACATCCTGACTGCCATGACCATTGACC 462
QY	392 GGTACTTTGCCCTCTGTCACCACTTCGACTGACAGTTGGAGAACAGAGTCAAGACCA 451
Db	463 GCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAAGTTCGGGAAGCGCTCCATGGCCA 522
QY	452 TCCGGATCAATTGGGCCCTTTGGGAGCTTCCTTTATCCTGGCATTGCTGTGGTCT 511
Db	523 CCCTGGTGAATGCTCTCTGTGGGCGCTCTCTCTTCATCATGATACACCCCTGTGTGGCTCT 582
QY	512 ACTCGAAGGTCAATCAAAATTAAAGACGGTGTTCAGAGTTGTGCTTTTGATTTTGACATCCC 571
Db	583 ACGCCAGGCTCAATCCCTTCCAGGGGGTGCTGTGGGCTGTGGCATCCGCTTGCCAAACC 642
QY	572 CTGACGATGACTCT 586
Db	643 CGGACACTGACCTCT 657

RESULT 12  
AQ492353/C

LOCUS	AQ492353	429 bp	DNA	linear	GSS 28-APR-1999							
DEFINITION	HS_5123_A2_E04_SP6E_RPCT-11 Human Male BAC Library Homo sapiens genomic clone Flates-899 Col-8 Row-1, genomic survey sequence.											
ACCESSION	AQ492353											
VERSION	AQ492353.1	GI:4691841										
KEYWORDS	GSS.											
SOURCE	Homo sapiens (human)											
ORGANISM	Homo sapiens											
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Homiidae; Homo.											
	1 (bases 1 to 429)											
	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.											
	sequence-tagged connectors: A sequence approach to mapping and scanning the human genome											
	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)											
TITLE												
JOURNAL												
MEDLINE	99380589											

PUBMED  
1049764  
COMMENT  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu  
Plate: 699 row: I column: 8  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 429.  
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/db\_xref="taxon:9606"  
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/notes="vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRII. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"  
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Query Match 11.7%; Score 120.2; DB 28; Length 429;  
Best Local Similarity 96.1%; Pred. No. 3.7e-19;  
Matches 122; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 269 TTCAACCAATGGCGGAGAGTGGTGGTGGGGGGCTCTCTGACCATCATCA 328  
DB 429 TTCAACCAATGGCGGAGAGTGGTGGTGGGGGGCTCTCTGACCATCATCA 370  
QY 329 CATCCCTGGTACTGTAAACCAATTTGCTGTAGTGCATCATGCTGAATGAGTGG 388  
DB 369 CATCCCTGGTACTGTAAACCAATTTGCTGTAGTGCATCATGCTGAATGAGTGG 310  
QY 389 ACAGGTA 395  
DB 309 ACAGGTA 303  
RESULT 13  
CF147812 723 bp mRNA linear EST 25-JUL-2003  
LOCUS AGENCOURT 14740188 NIH\_MGC\_145 Homo sapiens CDNA clone  
DEFINITION IMAGE:6971911 5', mRNA sequence.  
ACCESSION CF147812  
VERSION CF147812.1 GI:33244080  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 723)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRB102 row: C column: 06  
High quality sequence stop: 723.  
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/notes="vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed\_plates/IRB1.presv.dat a Note: this is a NIH\_MGC Library."  
ORIGIN  
Query Match 10.4%; Score 106.6; DB 14; Length 723;  
Best Local Similarity 54.1%; Pred. No. 9.7e-16;  
Matches 217; Conservative 0; Mismatches 184; Indels 0; Gaps 0;  
QY 186 CAGGAAAAAAGACAGTCCCTGACATCTATATCTGCAACCTGGCTGTGGCTATTTGGTCCA 245  
DB 221 CTGGTGCACCAACGTCCTCCGACATCTTCATCATCACTCTCGGTAGTAGATCTCTCTT 280  
QY 246 CATAGTTGGAATGCTTTCTTATTCACCATGGCCGAGGGGAGAGTGGTGGTGG 305  
DB 281 TCTCTCTGGGCAAGCCCTTCATGATCCACCACTCATGGCAATGGGTGGGCACTTTGG 340  
QY 306 GGGGCTCTCTGCAACCATCATCATCTGCTGATCTTTGTAACCAATTTGCTGTAGTGC 365  
DB 341 GGAGACCATGTGCACCTCTCATCGGCATGGATGCAATAGTCAGTTCACCACTCA 400  
QY 366 CATCATGCTGATAGTGTGGAGAGTACTTTGCTCTGCTCCCAACCATTTGCACTGAC 425  
DB 401 CATCTGACCCGCAATGGCCATTCACCGCTACCTGCGCCACTGTCCACCCCACTCTTCCAC 460  
QY 426 ACGTTGGAGAACAGGTACAAGACCATCCGATCAATTTGGGCTTTGGGCGAGCTTCTT 485  
DB 461 GAAGTTCGGAGAGCCCTCTGTGGCCACCTGTGCTGATCTGCTCTGTGGGCTCTCTT 520  
QY 486 TATCTCTGCAATGGCTGTCTGGTCTACTCGAAGGTCAATCAATTTAAAGACGGTGTGA 545  
DB 521 CATCAGCATCACCTGTGTGCTGTATGCCAGACTCATCCCTTCCAGAGGTGCACT 580  
QY 546 GAGTTGCTCTTTGATTGACATCCCTGACGATGATCTCT 586  
DB 581 GGGCTGGCGCATACGCTGCGCAACCCAGACACTGACCTCT 621

RESULT 14  
BX346496  
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DEFINITION CDNA clone CS0DD0011011 5-PRIME, mRNA sequence.  
ACCESSION BX346496  
VERSION BX346496.1 GI:30347416  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 988)

**AUTHORS** Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
**TITLE** Full-length cDNA libraries and normalization  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 10650.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0A0004ZH10\_A0368.l&cluster=10650.f.  
 Contact: Feng Liang Email: fliang@lifetech.com URL:  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID: CS0A0004ZH10\_A0368\_1.

**FEATURES**  
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 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

**ORIGIN**  
 Query Match 10.4%; Score 106.6; DB 13; Length 988;  
 Best Local Similarity 54.1%; Pred. No. 1e-15;  
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 QY 186 CAGGAAAAAAGTCCTGACATCTATATCTGCAACCTGGCTGGCTGATTGGTCCA 245  
 DB 182 CTGGTGCAACAGCTCCCGACATCTTCATCATCAACCTTCGGTAGTAGATCTCTCT 241  
 QY 246 CATAGTGGAAATGCTTTCTTATACCAATGGCCCGAGGGGAGTGGGTGGTGG 305  
 DB 242 TCTCCTGGGATGCCCTTCATGATCCACCACTCATGGGCAATGGGTGGGACATTGG 301  
 QY 306 GGGGCTCTCTGCACCATCATCATCTCCCTGGATCTGTGAACCAATTTGGCTGTAGTC 365  
 DB 302 GGAGACATGTGACCTCTATACGGCCATGGATGGATGCAATGATCAGTTACACGACCTA 361  
 QY 366 CATCATGACTGTATAGTGTGACAGGTACTTTGCCCTCTGTCACCAACCAATTTGCACTGAC 425  
 DB 362 CATCTGACCGCATGGCCATTCACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 421  
 QY 426 ACCTTGAGAACAGGTACAGACCATCCGGATCAATTTGGGCTTTGGGAGCTTCCTT 485  
 DB 422 GAAGTTCGGGAAGCCCTCTGTGGCCACCTGGTGTGATCTGCTCTGTGGGCTCTCTCTT 481  
 QY 486 TATCCTGGCATTCGCTCTGGTGTACTCGAAGTTCATCAAAATTTAAAGACGGTGTGCA 545  
 DB 482 CATCAGCATACCCCTGTGGTGTGTATGCCAGACTCATCCCTTCCAGAGGTGCACT 541  
 QY 546 GAGTTGTGCTTTTGTATGATCCCTGACGATGACTCT 586  
 DB 542 GGGCTGGGATACGCTGCGCCCAACCCAGACACTGACCTCT 582

**REFERENCE**  
**AUTHORS** Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
**TITLE** Full-length cDNA libraries and normalization  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 10650.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0A0004ZF10\_A0366.l&cluster=10650.f.  
 Contact: Feng Liang Email: fliang@lifetech.com URL:  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID: CS0A0004ZF10\_A0366\_1.

**FEATURES**  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="CS0DD001YN08"  
 /tissue\_type="NEUROBLASTOMA COT 50-NORMALIZED"  
 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

**ORIGIN**  
 Query Match 10.4%; Score 106.6; DB 13; Length 1012;  
 Best Local Similarity 54.1%; Pred. No. 1e-15;  
 Matches 217; Conservative 0; Mismatches 184; Indels 0; Gaps 0;  
 QY 186 CAGGAAAAAAGTCCTGACATCTATATCTGCAACCTGGCTGGCTGATTGGTCCA 245  
 DB 53 CTGGTGCAACAGCTCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCTCTT 112  
 QY 246 CATAGTGGAAATGCTTTCTTATACCAATGGCCCGAGGGGAGTGGGTGGTGG 305  
 DB 113 TCTCCTGGCATGCCCTTCATGATCCACCACTCATGGGCAATGGGTGGGACTTTGG 172  
 QY 306 GGGGCTCTCTGCACCATCATCATCTCCCTGGATCTGTGAACCAATTTGGCTGTAGTGC 365  
 DB 173 GGAGACCATGTGACCTCTCATCGGCCATGGATGCCAATAGTCAGTTACACGACCTA 232  
 QY 366 CATCATGACTGTATAGTGTGACAGGTACTTTGGCCTCTGTCACCAACCAATTTGCACTGAC 425  
 DB 233 CATCTGACCGCATGGCCATTCACCGCTACCTGGCCACTGTCCACCCCATCTCTTCCAC 292  
 QY 426 ACCTTGAGAACAGGTACAGACCATCCGGATCAATTTGGGCTTTGGGAGCTTCCTT 485  
 DB 293 GAAGTTCGGGAAGCCCTCTGTGGCCACCTGGTGTGATCTGCTCTGTGGGCTCTCTCTT 352  
 QY 486 TATCCTGGCATTCGCTCTGGTGTACTCGAAGGTGATCAAAATTTAAAGACGGTGTGCA 545  
 DB 353 CATCAGCATACCCCTGTGGTGTGTATGCCAGACTCATCCCTTCCAGAGGTGCACT 412  
 QY 546 GAGTTGTGCTTTTGTATGATCCCTGACGATGACTCT 586  
 DB 413 GGGCTGGGATACGCTGCGCCCAACCCAGACACTGACCTCT 453

Search completed: May 17, 2004, 21:29:09  
 Job time : 3090 secs

**RESULT 15**  
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**DEFINITION** BX367456 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens  
 cDNA clone CS0DD001YN08 5-PRIME, mRNA sequence.  
**ACCESSION** BX367456  
**VERSION** BX367456.1 GI:30447638  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

